



SEQUENCE LISTING

<110> BATTAGLINO, PETER
FEDER, JOHN N
MINTIER, GABE
NELSON, THOMAS C
RAMANATHAN, CHANDRA S
WESTPHAL, RYAN
CACACE, ANGELA
BARBER, LAUREN
HAWKEN, DONALD R
KORNACKER, MICHAEL G

<120> A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBMY8,
EXPRESSED HIGHLY IN BRAIN

<130> D0047NP

<140> 09/992,238

<141> 2001-11-13

<150> 60/317166

<151> 2001-09-04

<150> 60/308285

<151> 2001-07-27

<150> 60/268581

<151> 2001-02-14

<150> 60/248285

<151> 2000-11-14

<160> 102

<170> PatentIn Ver. 2.1

<210> 1

<211> 1527

<212> DNA

<213> Homo sapiens

<400> 1

atgacgtcca cctgcaccaa cagcacgcgc gagagtaaca gcagccacac gtgcatgccc 60
ctctccaaaa tgcccatcag cctggcccaac ggcacatccc gctcaaccgt gctgggttatc 120
ttcctcgccg cctctttcgt cggcaacata gtgctggcgc tagtggtgca gcgcaagccg 180
cagctgctgc aggtgaccaa ccgtttttatc tttaacctcc tcgtcaccga cctgctgcag 240
atttcgctcg tggccccctg ggtgggtggcc acctctgtgc ctctcttctg gccctcaac 300

```

agccacttct gcacggccct ggtagcctc acccacctgt tcgccttcgc cagcgtcaac 360
accattgtct tgggtgcagt ggatcgctac ttgtccatca tccaccctct ctccctacccg 420
tccaagatga cccagcgccg cggttacctg ctctcttatg gcacctggat tgtggccatc 480
ctgcagagca ctctccact ctacggctgg ggccaggctg cttttgatga gcgcaatgct 540
ctctgctcca tgatctgggg ggccagcccc agctacacta ttctcagcgt ggtgtccttc 600
atcgtcattc cactgattgt catgattgcc tgctactccg tgggtgttctg tgcagcccgg 660
aggcagcatg ctctgctgta caatgtcaag agacacagct tggaagtgcg agtcaaggac 720
tgtgtggaga atgaggatga agaggagca gagaagaagg aggagtcca ggatgagagt 780
gagtttcgcc gccagcatga aggtgaggtc aaggccaagg agggcagaat ggaagccaag 840
gacggcagcc tgaaggccaa ggaaggaagc acggggacca gtgagagtag tgtagaggcc 900
aggggcagcg aggaggtcag agagagcagc acggtggcca gcgacggcag catggagggt 960
aaggaaggca gcaccaaagt tgaggagaac agcatgaagg cagacaaggg tcgcacagag 1020
gtcaaccagt gcagcattga cttgggtgaa gatgacatgg agtttggtga agacgacatc 1080
aatttcagtg aggatgacgt cgaggcagtg aacatcccgg agagcctccc acccagtcgt 1140
cgtaacagca acagcaaccc tcctctgccc aggtgctacc agtgcaaagc tgctaaagtg 1200
atcttcatca tcattttctc ctatgtgcta tccctggggc cttactgctt tttagcagtc 1260
ctggccgtgt ggggtgatgt cgaaaccag gtacccagc ggggtgatcac cataatcatc 1320
tggtttttct tcctgcagtg ctgcatccac ccctatgtct atggctacat gcacaagacc 1380
attaagaagg aaatccagga catgctgaag aagttcttct gcaaggaaaa gccccgaaa 1440
gaagatagcc acccagacct gcccggaaca gaggggtggga ctgaaggcaa gattgtccct 1500
tcctacgatt ctgctacttt tccttga 1527

```

<210> 2

<211> 508

<212> PRT

<213> Homo sapiens

<400> 2

```

Met Thr Ser Thr Cys Thr Asn Ser Thr Arg Glu Ser Asn Ser Ser His
  1              5              10              15

Thr Cys Met Pro Leu Ser Lys Met Pro Ile Ser Leu Ala His Gly Ile
      20              25              30

Ile Arg Ser Thr Val Leu Val Ile Phe Leu Ala Ala Ser Phe Val Gly
      35              40              45

Asn Ile Val Leu Ala Leu Val Leu Gln Arg Lys Pro Gln Leu Leu Gln
      50              55              60

Val Thr Asn Arg Phe Ile Phe Asn Leu Leu Val Thr Asp Leu Leu Gln
      65              70              75              80

Ile Ser Leu Val Ala Pro Trp Val Val Ala Thr Ser Val Pro Leu Phe
      85              90              95

Trp Pro Leu Asn Ser His Phe Cys Thr Ala Leu Val Ser Leu Thr His

```

100

105

110

Leu Phe Ala Phe Ala Ser Val Asn Thr Ile Val Leu Val Ser Val Asp
 115 120 125

Arg Tyr Leu Ser Ile Ile His Pro Leu Ser Tyr Pro Ser Lys Met Thr
 130 135 140

Gln Arg Arg Gly Tyr Leu Leu Leu Tyr Gly Thr Trp Ile Val Ala Ile
 145 150 155 160

Leu Gln Ser Thr Pro Pro Leu Tyr Gly Trp Gly Gln Ala Ala Phe Asp
 165 170 175

Glu Arg Asn Ala Leu Cys Ser Met Ile Trp Gly Ala Ser Pro Ser Tyr
 180 185 190

Thr Ile Leu Ser Val Val Ser Phe Ile Val Ile Pro Leu Ile Val Met
 195 200 205

Ile Ala Cys Tyr Ser Val Val Phe Cys Ala Ala Arg Arg Gln His Ala
 210 215 220

Leu Leu Tyr Asn Val Lys Arg His Ser Leu Glu Val Arg Val Lys Asp
 225 230 235 240

Cys Val Glu Asn Glu Asp Glu Glu Gly Ala Glu Lys Lys Glu Glu Phe
 245 250 255

Gln Asp Glu Ser Glu Phe Arg Arg Gln His Glu Gly Glu Val Lys Ala
 260 265 270

Lys Glu Gly Arg Met Glu Ala Lys Asp Gly Ser Leu Lys Ala Lys Glu
 275 280 285

Gly Ser Thr Gly Thr Ser Glu Ser Ser Val Glu Ala Arg Gly Ser Glu
 290 295 300

Glu Val Arg Glu Ser Ser Thr Val Ala Ser Asp Gly Ser Met Glu Gly
 305 310 315 320

Lys Glu Gly Ser Thr Lys Val Glu Glu Asn Ser Met Lys Ala Asp Lys
 325 330 335

Gly Arg Thr Glu Val Asn Gln Cys Ser Ile Asp Leu Gly Glu Asp Asp
 340 345 350

Met Glu Phe Gly Glu Asp Asp Ile Asn Phe Ser Glu Asp Asp Val Glu

355	360	365
Ala Val Asn Ile Pro Glu Ser Leu Pro Pro Ser Arg Arg Asn Ser Asn		
370	375	380
Ser Asn Pro Pro Leu Pro Arg Cys Tyr Gln Cys Lys Ala Ala Lys Val		
385	390	395 400
Ile Phe Ile Ile Ile Phe Ser Tyr Val Leu Ser Leu Gly Pro Tyr Cys		
405	410	415
Phe Leu Ala Val Leu Ala Val Trp Val Asp Val Glu Thr Gln Val Pro		
420	425	430
Gln Trp Val Ile Thr Ile Ile Ile Trp Leu Phe Phe Leu Gln Cys Cys		
435	440	445
Ile His Pro Tyr Val Tyr Gly Tyr Met His Lys Thr Ile Lys Lys Glu		
450	455	460
Ile Gln Asp Met Leu Lys Lys Phe Phe Cys Lys Glu Lys Pro Pro Lys		
465	470	475 480
Glu Asp Ser His Pro Asp Leu Pro Gly Thr Glu Gly Gly Thr Glu Gly		
485	490	495
Lys Ile Val Pro Ser Tyr Asp Ser Ala Thr Phe Pro		
500	505	

<210> 3
 <211> 31
 <212> DNA
 <213> Homo sapiens

<400> 3
 gcaacctgtc tcacgccctc tggctgttgc c 31

<210> 4
 <211> 22
 <212> DNA
 <213> Homo sapiens

<400> 4
 agttagttct aaggcaaacc tt 22

<210> 5
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: HGPRBMY8
sense primer

<400> 5
ggccgaattc gcaacctgtc tcacgccctc tgg 33

<210> 6
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: HGPRBMY8
anti-sense primer

<400> 6
ggccgaattc ggacagttca aggtttgcct tagaac 36

<210> 7
<211> 490
<212> PRT
<213> Gallus gallus

<400> 7
Met His Asn Leu Ser Ala Gln Pro Trp Gln Ala Lys Met Ala Asn Leu
1 5 10 15
Thr Tyr Asp Asn Val Thr Leu Ser Asn Arg Ser Glu Val Ala Ile Gln
20 25 30
Pro Pro Thr Asn Tyr Lys Thr Val Glu Leu Val Phe Ile Ala Thr Val
35 40 45
Thr Gly Ser Leu Ser Leu Val Thr Val Val Gly Asn Ile Leu Val Met
50 55 60
Leu Ser Ile Lys Val Asn Arg Gln Leu Gln Thr Val Asn Asn Tyr Phe
65 70 75 80
Leu Phe Ser Leu Ala Cys Ala Asp Leu Ile Ile Gly Val Phe Ser Met

85								90				95					
Asn	Leu	Tyr	Thr	Val	Tyr	Ile	Ile	Lys	Gly	Tyr	Trp	Pro	Leu	Gly	Ala		
100								105				110					
Val	Val	Cys	Asp	Leu	Trp	Leu	Ala	Leu	Asp	Tyr	Val	Val	Ser	Asn	Ala		
115								120				125					
Ser	Val	Met	Asn	Leu	Leu	Ile	Ile	Ser	Phe	Asp	Arg	Tyr	Phe	Cys	Val		
130								135				140					
Thr	Lys	Pro	Leu	Thr	Tyr	Pro	Ala	Arg	Arg	Thr	Thr	Lys	Met	Ala	Gly		
145								150				155				160	
Leu	Met	Ile	Ala	Ala	Ala	Trp	Ile	Leu	Ser	Phe	Ile	Leu	Trp	Ala	Pro		
165								170				175					
Ala	Ile	Leu	Phe	Trp	Gln	Phe	Ile	Val	Gly	Lys	Arg	Thr	Val	His	Glu		
180								185				190					
Arg	Glu	Cys	Tyr	Ile	Gln	Phe	Leu	Ser	Asn	Pro	Ala	Val	Thr	Phe	Gly		
195								200				205					
Thr	Ala	Ile	Ala	Ala	Phe	Tyr	Leu	Pro	Val	Val	Ile	Met	Thr	Val	Leu		
210								215				220					
Tyr	Ile	His	Ile	Ser	Leu	Ala	Ser	Arg	Ser	Arg	Val	Arg	Arg	His	Lys		
225								230				235				240	
Pro	Glu	Ser	Arg	Lys	Glu	Arg	Lys	Gly	Lys	Ser	Leu	Ser	Phe	Phe	Lys		
245								250				255					
Ala	Pro	Pro	Val	Lys	Gln	Asn	Asn	Asn	Asn	Ser	Pro	Lys	Arg	Ala	Val		
260								265				270					
Glu	Val	Lys	Glu	Glu	Val	Arg	Asn	Gly	Lys	Val	Asp	Asp	Gln	Pro	Ser		
275								280				285					
Ala	Gln	Thr	Glu	Ala	Thr	Gly	Gln	Gln	Glu	Glu	Lys	Glu	Thr	Ser	Asn		
290								295				300					
Glu	Ser	Ser	Thr	Val	Ser	Met	Thr	Gln	Thr	Thr	Lys	Asp	Lys	Pro	Thr		
305								310				315				320	
Thr	Glu	Ile	Leu	Pro	Ala	Gly	Gln	Gly	Gln	Ser	Pro	Ala	His	Pro	Arg		
325								330				335					
Val	Asn	Pro	Thr	Ser	Lys	Trp	Ser	Lys	Ile	Lys	Ile	Val	Thr	Lys	Gln		

340	345	350
Thr Gly Thr Glu Ser Val Thr Ala Ile Glu Ile Val Pro Ala Lys Ala		
355	360	365
Gly Ala Ser Asp His Asn Ser Leu Ser Asn Ser Arg Pro Ala Asn Val		
370	375	380
Ala Arg Lys Phe Ala Ser Ile Ala Arg Ser Gln Val Arg Lys Lys Arg		
385	390	395 400
Gln Met Ala Ala Arg Glu Lys Lys Val Thr Arg Thr Ile Phe Ala Ile		
405	410	415
Leu Leu Ala Phe Ile Leu Thr Trp Thr Pro Tyr Asn Val Met Val Leu		
420	425	430
Ile Asn Thr Phe Cys Glu Thr Cys Val Pro Glu Thr Val Trp Ser Ile		
435	440	445
Gly Tyr Trp Leu Cys Tyr Val Asn Ser Thr Ile Asn Pro Ala Cys Tyr		
450	455	460
Ala Leu Cys Asn Ala Thr Phe Lys Lys Thr Phe Lys His Leu Leu Met		
465	470	475 480
Cys Gln Tyr Arg Asn Ile Gly Thr Ala Arg		
485	490	

<210> 8

<211> 488

<212> PRT

<213> Caenorhabditis elegans

<400> 8

Met Cys Phe Ala Glu Lys Gly Glu Gly Ala Gly Glu Asp Val Asp His
1 5 10 15
His Ser Leu Phe Cys Pro Lys Lys Leu Val Gly Asn Leu Lys Gly Phe
20 25 30
Ile Arg Asn Gln Tyr His Gln His Glu Thr Ile Gln Ile Leu Lys Gly
35 40 45
Ser Ala Leu Phe Leu Leu Val Leu Trp Thr Ile Phe Ala Asn Ser Leu
50 55 60

Val Phe Ile Val Leu Tyr Lys Asn Pro Arg Leu Gln Thr Val Pro Asn
65 70 75 80

Leu Leu Val Gly Asn Leu Ala Phe Ser Asp Leu Ala Leu Gly Leu Ile
85 90 95

Val Leu Pro Leu Ser Ser Val Tyr Ala Ile Ala Gly Glu Trp Val Phe
100 105 110

Pro Asp Ala Leu Cys Glu Val Phe Val Ser Ala Asp Ile Leu Cys Ser
115 120 125

Thr Ala Ser Ile Trp Asn Leu Ser Ile Val Gly Leu Asp Arg Tyr Trp
130 135 140

Ala Ile Thr Ser Pro Val Ala Tyr Met Ser Lys Arg Asn Lys Arg Thr
145 150 155 160

Ala Gly Ile Met Ile Leu Ser Val Trp Ile Ser Ser Ala Leu Ile Ser
165 170 175

Leu Ala Pro Leu Leu Gly Trp Lys Gln Thr Ala Gln Thr Pro Asn Leu
180 185 190

Ile Tyr Glu Lys Asn Asn Thr Val Arg Gln Cys Thr Phe Leu Asp Leu
195 200 205

Pro Ser Tyr Thr Val Tyr Ser Ala Thr Gly Ser Phe Phe Ile Pro Thr
210 215 220

Leu Leu Met Phe Phe Val Tyr Phe Lys Ile Tyr Gln Ala Phe Ala Lys
225 230 235 240

His Arg Ala Arg Gln Ile Tyr Arg Gln Lys Val Ile Arg Lys His Ile
245 250 255

Glu Ser Thr Ile Leu His Glu Ile Ser His Val Leu Pro Thr Ser Asp
260 265 270

Glu Phe Ala Lys Glu Glu Glu Glu Glu Glu Asp Ser Glu Ser Ser Gly
275 280 285

Gln Val Glu Asn Gly Leu Gly Asn Gly Asn Asp Ala Ile Ile Glu Glu
290 295 300

Asp Glu Cys Glu Asp Glu Asp Ser Asp Glu Lys Arg Asp Asp His Thr
305 310 315 320

Ser Met Thr Thr Val Thr Ala Thr Val Thr Gly Pro Thr Glu Ala Pro
 325 330 335

Tyr Met Lys Arg Glu Ala Lys Ile Ser Lys Ser Val Pro Ile Glu Lys
 340 345 350

Glu Ser Ala Ile Gln Lys Arg Glu Ala Lys Pro Met Arg Ser Val Met
 355 360 365

Ala Ile Ser Tyr Glu Lys Val Lys Arg His Lys Asn Arg Lys Glu Arg
 370 375 380

Ile Tyr Arg Lys Ser Leu Gln Arg Lys Pro Lys Ala Ile Ser Ala Ala
 385 390 395 400

Lys Glu Arg Arg Gly Val Lys Val Leu Gly Ile Ile Leu Gly Cys Phe
 405 410 415

Thr Val Cys Trp Ala Pro Phe Phe Thr Met Tyr Val Leu Val Gln Phe
 420 425 430

Cys Lys Asp Cys Ser Pro Asn Ala His Ile Glu Met Phe Ile Thr Trp
 435 440 445

Leu Gly Tyr Ser Asn Ser Ala Met Asn Pro Ile Ile Tyr Thr Val Phe
 450 455 460

Asn Arg Asp Tyr Gln Ile Ala Leu Lys Arg Leu Phe Thr Ser Glu Lys
 465 470 475 480

Lys Pro Ser Ser Thr Ser Arg Val
 485

<210> 9

<211> 423

<212> PRT

<213> Homo sapiens

<400> 9

Met Asp Leu Arg Ala Thr Ser Ser Asn Asp Ser Asn Ala Thr Ser Gly
 1 5 10 15

Tyr Ser Asp Thr Ala Ala Val Asp Trp Asp Glu Gly Glu Asn Ala Thr
 20 25 30

Gly Ser Gly Ser Leu Pro Asp Pro Glu Leu Ser Tyr Gln Ile Ile Thr
 35 40 45



Ser Leu Phe Leu Gly Ala Leu Ile Leu Cys Ser Ile Phe Gly Asn Ser
50 55 60

Cys Val Val Ala Ala Ile Ala Leu Glu Arg Ser Leu Gln Asn Val Ala
65 70 75 80

Asn Tyr Leu Ile Gly Ser Leu Ala Val Thr Asp Leu Met Val Ser Val
85 90 95

Leu Val Leu Pro Met Ala Ala Leu Tyr Gln Val Leu Asn Lys Trp Thr
100 105 110

Leu Gly Gln Asp Ile Cys Asp Leu Phe Ile Ala Leu Asp Val Leu Cys
115 120 125

Cys Thr Ser Ser Ile Leu His Leu Cys Ala Ile Ala Leu Asp Arg Tyr
130 135 140

Trp Ala Ile Thr Asp Pro Ile Asp Tyr Val Asn Lys Arg Thr Pro Arg
145 150 155 160

Arg Ala Ala Val Leu Ile Ser Val Thr Trp Leu Ile Gly Phe Ser Ile
165 170 175

Ser Ile Pro Pro Met Leu Gly Trp Arg Ser Ala Glu Asp Arg Ala Asn
180 185 190

Pro Asp Ala Cys Ile Ile Ser Gln Asp Pro Gly Tyr Thr Ile Tyr Ser
195 200 205

Thr Phe Gly Ala Phe Tyr Ile Pro Leu Ile Leu Met Leu Val Leu Tyr
210 215 220

Gly Arg Ile Phe Lys Ala Ala Arg Phe Arg Ile Arg Lys Thr Val Lys
225 230 235 240

Lys Thr Glu Lys Ala Lys Ala Ser Asp Met Cys Leu Thr Leu Ser Pro
245 250 255

Ala Val Phe His Lys Arg Ala Asn Gly Asp Ala Val Ser Ala Glu Trp
260 265 270

Lys Arg Gly Tyr Lys Phe Lys Pro Ser Ser Pro Cys Ala Asn Gly Ala
275 280 285

Val Arg His Gly Glu Glu Met Glu Ser Leu Glu Ile Ile Glu Val Asn
290 295 300

Ser Asn Ser Lys Thr His Leu Pro Leu Pro Asn Thr Pro Gln Ser Ser
 305 310 315 320

Ser His Glu Asn Ile Asn Glu Lys Thr Thr Gly Thr Arg Arg Lys Ile
 325 330 335

Ala Leu Ala Arg Glu Arg Lys Thr Val Lys Thr Leu Gly Ile Ile Met
 340 345 350

Gly Thr Phe Ile Phe Cys Trp Leu Pro Phe Phe Ile Val Ala Leu Val
 355 360 365

Leu Pro Phe Cys Ala Glu Asn Cys Tyr Met Pro Glu Trp Leu Gly Ala
 370 375 380

Val Ile Asn Trp Leu Gly Tyr Ser Asn Ser Leu Leu Asn Pro Ile Ile
 385 390 395 400

Tyr Ala Tyr Phe Asn Lys Asp Phe Gln Ser Ala Phe Lys Lys Ile Leu
 405 410 415

Arg Cys Lys Phe His Arg His
 420

<210> 10

<211> 421

<212> PRT

<213> Mus musculus

<400> 10

Met Asp Met Phe Ser Leu Gly Gln Gly Asn Asn Thr Thr Thr Ser Leu
 1 5 10 15

Glu Pro Phe Gly Thr Gly Gly Asn Asp Thr Gly Leu Ser Asn Val Thr
 20 25 30

Phe Ser Tyr Gln Val Ile Thr Ser Leu Leu Leu Gly Thr Leu Ile Phe
 35 40 45

Cys Ala Val Leu Gly Asn Ala Cys Val Val Ala Ala Ile Ala Leu Glu
 50 55 60

Arg Ser Leu Gln Asn Val Ala Asn Tyr Leu Ile Gly Ser Leu Ala Val
 65 70 75 80

Thr Asp Leu Met Val Ser Val Leu Val Leu Pro Met Ala Ala Leu Tyr

				85				90				95			
Gln	Val	Leu	Asn	Lys	Trp	Thr	Leu	Gly	Gln	Val	Thr	Cys	Asp	Leu	Phe
100				105				110							
Ile	Ala	Leu	Asp	Val	Leu	Cys	Cys	Thr	Ser	Ser	Ile	Leu	His	Leu	Cys
115				120				125							
Ala	Ile	Ala	Leu	Asp	Arg	Tyr	Trp	Ala	Ile	Thr	Asp	Pro	Ile	Asp	Tyr
130				135				140							
Val	Asn	Lys	Arg	Thr	Pro	Arg	Arg	Ala	Ala	Ala	Leu	Ile	Ser	Leu	Thr
145				150				155				160			
Trp	Leu	Ile	Gly	Phe	Leu	Ile	Ser	Ile	Pro	Pro	Met	Leu	Gly	Trp	Arg
165				170				175							
Ala	Pro	Glu	Asp	Arg	Ser	Asn	Pro	Asn	Glu	Cys	Thr	Ile	Ser	Lys	Asp
180				185				190							
His	Gly	Tyr	Thr	Ile	Tyr	Ser	Thr	Phe	Gly	Ala	Phe	Tyr	Ile	Pro	Leu
195				200				205							
Leu	Leu	Met	Leu	Val	Leu	Tyr	Gly	Arg	Ile	Phe	Arg	Ala	Ala	Arg	Phe
210				215				220							
Arg	Ile	Arg	Lys	Thr	Val	Lys	Lys	Val	Glu	Lys	Lys	Gly	Ala	Gly	Thr
225				230				235				240			
Ser	Phe	Gly	Thr	Ser	Ser	Ala	Pro	Pro	Pro	Lys	Lys	Ser	Leu	Asn	Gly
245				250				255							
Gln	Pro	Gly	Ser	Gly	Asp	Cys	Arg	Arg	Ser	Ala	Glu	Asn	Arg	Ala	Val
260				265				270							
Gly	Thr	Pro	Cys	Ala	Asn	Gly	Ala	Val	Arg	Gln	Gly	Glu	Asp	Asp	Ala
275				280				285							
Thr	Leu	Glu	Val	Ile	Glu	Val	His	Arg	Val	Gly	Asn	Ser	Lys	Gly	Asp
290				295				300							
Leu	Pro	Leu	Pro	Ser	Glu	Ser	Gly	Ala	Thr	Ser	Tyr	Val	Pro	Ala	Cys
305				310				315				320			
Leu	Glu	Arg	Lys	Asn	Glu	Arg	Thr	Ala	Glu	Ala	Lys	Arg	Lys	Met	Ala
325				330				335							
Leu	Ala	Arg	Glu	Arg	Lys	Thr	Val	Lys	Thr	Leu	Gly	Ile	Ile	Met	Glu

340	345	350
Thr Phe Ile Leu Cys Trp Leu Pro Phe Phe Ile Val Ala Leu Val Leu		
355	360	365
Pro Phe Cys Glu Ser Ser Cys His Met Pro Glu Leu Leu Gly Ala Ile		
370	375	380
Ile Asn Trp Leu Gly Tyr Ser Asn Ser Leu Leu Asn Pro Val Ile Tyr		
385	390	395 400
Ala Tyr Phe Asn Lys Asp Phe Gln Asn Ala Phe Lys Lys Ile Ile Lys		
405	410	415
Cys Lys Phe Cys Arg		
420		
<210> 11		
<211> 423		
<212> PRT		
<213> Fugu rubripes		
<400> 11		
Met Asp Leu Arg Ala Thr Ser Ser Asn Asp Ser Asn Ala Thr Ser Gly		
1	5	10 15
Tyr Ser Asp Thr Ala Ala Val Asp Trp Asp Glu Gly Glu Asn Ala Thr		
20	25	30
Gly Ser Gly Ser Leu Pro Asp Pro Glu Leu Ser Tyr Gln Ile Ile Thr		
35	40	45
Ser Leu Phe Leu Gly Ala Leu Ile Leu Cys Ser Ile Phe Gly Asn Ser		
50	55	60
Cys Val Val Ala Ala Ile Ala Leu Glu Arg Ser Leu Gln Asn Val Ala		
65	70	75 80
Asn Tyr Leu Ile Gly Ser Leu Ala Val Thr Asp Leu Met Val Ser Val		
85	90	95
Leu Val Leu Pro Met Ala Ala Leu Tyr Gln Val Leu Asn Lys Trp Thr		
100	105	110
Leu Gly Gln Asp Ile Cys Asp Leu Phe Ile Ala Leu Asp Val Leu Cys		
115	120	125

Cys Thr Ser Ser Ile Leu His Leu Cys Ala Ile Ala Leu Asp Arg Tyr
 130 135 140

Trp Ala Ile Thr Asp Pro Ile Asp Tyr Val Asn Lys Arg Thr Pro Arg
 145 150 155 160

Arg Ala Ala Val Leu Ile Ser Val Thr Trp Leu Ile Gly Phe Ser Ile
 165 170 175

Ser Ile Pro Pro Met Leu Gly Trp Arg Ser Ala Glu Asp Arg Ala Asn
 180 185 190

Pro Asp Ala Cys Ile Ile Ser Gln Asp Pro Gly Tyr Thr Ile Tyr Ser
 195 200 205

Thr Phe Gly Ala Phe Tyr Ile Pro Leu Ile Leu Met Leu Val Leu Tyr
 210 215 220

Gly Arg Ile Phe Lys Ala Ala Arg Phe Arg Ile Arg Lys Thr Val Lys
 225 230 235 240

Lys Thr Glu Lys Ala Lys Ala Ser Asp Met Cys Leu Thr Leu Ser Pro
 245 250 255

Ala Val Phe His Lys Arg Ala Asn Gly Asp Ala Val Ser Ala Glu Trp
 260 265 270

Lys Arg Gly Tyr Lys Phe Lys Pro Ser Ser Pro Cys Ala Asn Gly Ala
 275 280 285

Val Arg His Gly Glu Glu Met Glu Ser Leu Glu Ile Ile Glu Val Asn
 290 295 300

Ser Asn Ser Lys Thr His Leu Pro Leu Pro Asn Thr Pro Gln Ser Ser
 305 310 315 320

Ser His Glu Asn Ile Asn Glu Lys Thr Thr Gly Thr Arg Arg Lys Ile
 325 330 335

Ala Leu Ala Arg Glu Arg Lys Thr Val Lys Thr Leu Gly Ile Ile Met
 340 345 350

Gly Thr Phe Ile Phe Cys Trp Leu Pro Phe Phe Ile Val Ala Leu Val
 355 360 365

Leu Pro Phe Cys Ala Glu Asn Cys Tyr Met Pro Glu Trp Leu Gly Ala
 370 375 380

Val Ile Asn Trp Leu Gly Tyr Ser Asn Ser Leu Leu Asn Pro Ile Ile
 385 390 395 400

Tyr Ala Tyr Phe Asn Lys Asp Phe Gln Ser Ala Phe Lys Lys Ile Leu
 405 410 415

Arg Cys Lys Phe His Arg His
 420

<210> 12
 <211> 509
 <212> PRT
 <213> *Lymnaea stagnalis*

<400> 12
 Met Ala Asn Phe Thr Phe Gly Asp Leu Ala Leu Asp Val Ala Arg Met
 1 5 10 15

Gly Gly Leu Ala Ser Thr Pro Ser Gly Leu Arg Ser Thr Gly Leu Thr
 20 25 30

Thr Pro Gly Leu Ser Pro Thr Gly Leu Val Thr Ser Asp Phe Asn Asp
 35 40 45

Ser Tyr Gly Leu Thr Gly Gln Phe Ile Asn Gly Ser His Ser Ser Arg
 50 55 60

Ser Arg Asp Asn Ala Ser Ala Asn Asp Thr Ser Ala Thr Asn Met Thr
 65 70 75 80

Asp Asp Arg Tyr Trp Ser Leu Thr Val Tyr Ser His Glu His Leu Val
 85 90 95

Leu Thr Ser Val Ile Leu Gly Leu Phe Val Leu Cys Cys Ile Ile Gly
 100 105 110

Asn Cys Phe Val Ile Ala Ala Val Met Leu Glu Arg Ser Leu His Asn
 115 120 125

Val Ala Asn Tyr Leu Ile Leu Ser Leu Ala Val Ala Asp Leu Met Val
 130 135 140

Ala Val Leu Val Met Pro Leu Ser Val Val Ser Glu Ile Ser Lys Val
 145 150 155 160

Trp Phe Leu His Ser Glu Val Cys Asp Met Trp Ile Ser Val Asp Val
 165 170 175

Leu Cys Cys Thr Ala Ser Ile Leu His Leu Val Ala Ile Ala Met Asp
 180 185 190

Arg Tyr Trp Ala Val Thr Ser Ile Asp Tyr Ile Arg Arg Arg Ser Ala
 195 200 205

Arg Arg Ile Leu Leu Met Ile Met Val Val Trp Ile Val Ala Leu Phe
 210 215 220

Ile Ser Ile Pro Pro Leu Phe Gly Trp Arg Asp Pro Asn Asn Asp Pro
 225 230 235 240

Asp Lys Thr Gly Thr Cys Ile Ile Ser Gln Asp Lys Gly Tyr Thr Ile
 245 250 255

Phe Ser Thr Val Gly Ala Phe Tyr Leu Pro Met Leu Val Met Met Ile
 260 265 270

Ile Tyr Ile Arg Ile Trp Leu Val Ala Arg Ser Arg Ile Arg Lys Asp
 275 280 285

Lys Phe Gln Met Thr Lys Ala Arg Leu Lys Thr Glu Glu Thr Thr Leu
 290 295 300

Val Ala Ser Pro Lys Thr Glu Tyr Ser Val Val Ser Asp Cys Asn Gly
 305 310 315 320

Cys Asn Ser Pro Asp Ser Thr Thr Glu Lys Lys Lys Arg Arg Ala Pro
 325 330 335

Phe Lys Ser Tyr Gly Cys Ser Pro Arg Pro Glu Arg Lys Lys Asn Arg
 340 345 350

Ala Lys Lys Leu Pro Glu Asn Ala Asn Gly Val Asn Ser Asn Ser Ser
 355 360 365

Ser Ser Glu Arg Leu Lys Gln Ile Gln Ile Glu Thr Ala Glu Ala Phe
 370 375 380

Ala Asn Gly Cys Ala Glu Glu Ala Ser Ile Ala Met Leu Glu Arg Gln
 385 390 395 400

Cys Asn Asn Gly Lys Lys Ile Ser Ser Asn Asp Thr Pro Tyr Ser Arg
 405 410 415

Thr Arg Glu Lys Leu Glu Leu Lys Arg Glu Arg Lys Ala Ala Arg Thr
 420 425 430

Leu Ala Ile Ile Thr Gly Ala Phe Leu Ile Cys Trp Leu Pro Phe Phe
435 440 445

Ile Ile Ala Leu Ile Gly Pro Phe Val Asp Pro Glu Gly Ile Pro Pro
450 455 460

Phe Ala Arg Ser Phe Val Leu Trp Leu Gly Tyr Phe Asn Ser Leu Leu
465 470 475 480

Asn Pro Ile Ile Tyr Thr Ile Phe Ser Pro Glu Phe Arg Ser Ala Phe
485 490 495

Gln Lys Ile Leu Phe Gly Lys Tyr Arg Arg Gly His Arg
500 505

<210> 13

<211> 572

<212> PRT

<213> Homo sapiens

<400> 13

Met Thr Phe Arg Asp Leu Leu Ser Val Ser Phe Glu Gly Pro Arg Pro
1 5 10 15

Asp Ser Ser Ala Gly Gly Ser Ser Ala Gly Gly Gly Gly Gly Ser Ala
20 25 30

Gly Gly Ala Ala Pro Ser Glu Gly Pro Ala Val Gly Gly Val Pro Gly
35 40 45

Gly Ala Gly Gly Gly Gly Gly Val Val Gly Ala Gly Ser Gly Glu Asp
50 55 60

Asn Arg Ser Ser Ala Gly Glu Pro Gly Ser Ala Gly Ala Gly Gly Asp
65 70 75 80

Val Asn Gly Thr Ala Ala Val Gly Gly Leu Val Val Ser Ala Gln Gly
85 90 95

Val Gly Val Gly Val Phe Leu Ala Ala Phe Ile Leu Met Ala Val Ala
100 105 110

Gly Asn Leu Leu Val Ile Leu Ser Val Ala Cys Asn Arg His Leu Gln
115 120 125

Thr Val Thr Asn Tyr Phe Ile Val Asn Leu Ala Val Ala Asp Leu Leu

130		135		140
Leu Ser Ala Thr Val	Leu Pro Phe Ser Ala Thr	Met Glu Val Leu Gly		
145	150	155	160	
Phe Trp Ala Phe Gly Arg Ala Phe Cys Asp Val	Trp Ala Ala Val Asp			
	165	170	175	
Val Leu Cys Cys Thr Ala Ser Ile Leu Ser Leu Cys Thr Ile Ser Val				
	180	185	190	
Asp Arg Tyr Val Gly Val Arg His Ser Leu Lys Tyr Pro Ala Ile Met				
	195	200	205	
Thr Glu Arg Lys Ala Ala Ala Ile Leu Ala Leu Leu Trp Val Val Ala				
	210	215	220	
Leu Val Val Ser Val Gly Pro Leu Leu Gly Trp Lys Glu Pro Val Pro				
	225	230	235	240
Pro Asp Glu Arg Phe Cys Gly Ile Thr Glu Glu Ala Gly Tyr Ala Val				
	245	250	255	
Phe Ser Ser Val Cys Ser Phe Tyr Leu Pro Met Ala Val Ile Val Val				
	260	265	270	
Met Tyr Cys Arg Val Tyr Val Val Ala Arg Ser Thr Thr Arg Ser Leu				
	275	280	285	
Glu Ala Gly Val Lys Arg Glu Arg Gly Lys Ala Ser Glu Val Val Leu				
	290	295	300	
Arg Ile His Cys Arg Gly Ala Ala Thr Gly Ala Asp Gly Ala His Gly				
	305	310	315	320
Met Arg Ser Ala Lys Gly His Thr Phe Arg Ser Ser Leu Ser Val Arg				
	325	330	335	
Leu Leu Lys Phe Ser Arg Glu Lys Lys Ala Ala Lys Thr Leu Ala Ile				
	340	345	350	
Val Val Gly Val Phe Val Leu Cys Trp Phe Pro Phe Phe Phe Val Leu				
	355	360	365	
Pro Leu Gly Ser Leu Phe Pro Gln Leu Lys Pro Ser Glu Gly Val Phe				
	370	375	380	
Lys Val Ile Phe Trp Leu Gly Tyr Phe Asn Ser Cys Val Asn Pro Leu				

Gly Pro Glu Gly Pro Ala Val Gly Gly Val Pro Gly Ala Thr Gly Gly
 35 40 45
 Ser Ala Val Val Gly Thr Gly Ser Gly Glu Asp Asn Gln Ser Ser Thr
 50 55 60
 Ala Glu Ala Gly Ala Ala Ala Ser Gly Glu Val Asn Gly Ser Ala Ala
 65 70 75 80
 Val Gly Gly Leu Val Val Ser Ala Gln Gly Val Gly Val Gly Val Phe
 85 90 95
 Leu Ala Ala Phe Ile Leu Thr Ala Val Ala Gly Asn Leu Leu Val Ile
 100 105 110
 Leu Ser Val Ala Cys Asn Arg His Leu Gln Thr Val Thr Asn Tyr Phe
 115 120 125
 Ile Val Asn Leu Ala Val Ala Asp Leu Leu Leu Ser Ala Ala Val Leu
 130 135 140
 Pro Phe Ser Ala Thr Met Glu Val Leu Gly Phe Trp Pro Phe Gly Arg
 145 150 155 160
 Thr Phe Cys Asp Val Trp Ala Ala Val Asp Val Leu Cys Cys Thr Ala
 165 170 175
 Ser Ile Leu Ser Leu Cys Thr Ile Ser Val Asp Arg Tyr Val Gly Val
 180 185 190
 Arg His Ser Leu Lys Tyr Pro Ala Ile Met Thr Glu Arg Lys Ala Ala
 195 200 205
 Ala Ile Leu Ala Leu Leu Trp Ala Val Ala Leu Val Val Ser Val Gly
 210 215 220
 Pro Leu Leu Gly Trp Lys Glu Pro Val Pro Pro Asp Glu Arg Phe Cys
 225 230 235 240
 Gly Ile Thr Glu Glu Val Gly Tyr Ala Ile Phe Ser Ser Val Cys Ser
 245 250 255
 Phe Tyr Leu Pro Met Ala Val Ile Val Val Met Tyr Cys Arg Val Tyr
 260 265 270
 Val Val Ala Arg Ser Thr Thr Arg Ser Leu Glu Ala Gly Ile Lys Arg
 275 280 285

Glu	Pro	Gly	Lys	Ala	Ser	Glu	Val	Val	Leu	Arg	Ile	His	Cys	Arg	Gly	290	295	300	
Ala	Ala	Thr	Ser	Ala	Lys	Gly	Asn	Pro	Gly	Thr	Gln	Ser	Ser	Lys	Gly	305	310	315	320
His	Thr	Leu	Arg	Ser	Ser	Leu	Ser	Val	Arg	Leu	Leu	Lys	Phe	Ser	Arg	325	330	335	
Glu	Lys	Lys	Ala	Ala	Lys	Thr	Leu	Ala	Ile	Val	Val	Gly	Val	Phe	Val	340	345	350	
Leu	Cys	Trp	Phe	Pro	Phe	Phe	Phe	Val	Leu	Pro	Leu	Gly	Ser	Leu	Phe	355	360	365	
Pro	Gln	Leu	Lys	Pro	Ser	Glu	Gly	Val	Phe	Lys	Val	Ile	Phe	Trp	Leu	370	375	380	
Gly	Tyr	Phe	Asn	Ser	Cys	Val	Asn	Pro	Leu	Ile	Tyr	Pro	Cys	Ser	Ser	385	390	395	400
Arg	Glu	Phe	Lys	Arg	Ala	Phe	Leu	Arg	Leu	Leu	Arg	Cys	Gln	Cys	Arg	405	410	415	
Arg	Arg	Arg	Arg	Arg	Leu	Trp	Pro	Ser	Leu	Arg	Pro	Pro	Leu	Ala	Ser	420	425	430	
Leu	Asp	Arg	Arg	Pro	Ala	Leu	Arg	Leu	Cys	Pro	Gln	Pro	Ala	His	Arg	435	440	445	
Thr	Pro	Arg	Gly	Ser	Pro	Ser	Pro	His	Cys	Thr	Pro	Arg	Pro	Gly	Leu	450	455	460	
Arg	Arg	His	Ala	Gly	Gly	Ala	Gly	Phe	Gly	Leu	Arg	Pro	Ser	Lys	Ala	465	470	475	480
Ser	Leu	Arg	Leu	Arg	Glu	Trp	Arg	Leu	Leu	Gly	Pro	Leu	Gln	Arg	Pro	485	490	495	
Thr	Thr	Gln	Leu	Arg	Ala	Lys	Val	Ser	Ser	Leu	Ser	His	Lys	Phe	Arg	500	505	510	
Ser	Gly	Gly	Ala	Arg	Arg	Ala	Glu	Thr	Ala	Cys	Ala	Leu	Arg	Ser	Glu	515	520	525	
Val	Glu	Ala	Val	Ser	Leu	Asn	Val	Pro	Gln	Asp	Gly	Ala	Glu	Ala	Val	530	535	540	

Ile Cys Gln Ala Tyr Glu Pro Gly Asp Leu Ser Asn Leu Arg Glu Thr
545 550 555 560

Asp Ile

<210> 15

<211> 499

<212> PRT

<213> Homo sapiens

<400> 15

Met Val Phe Leu Ser Gly Asn Ala Ser Asp Ser Ser Asn Cys Thr Gln
1 5 10 15

Pro Pro Ala Pro Val Asn Ile Ser Lys Ala Ile Leu Leu Gly Val Ile
20 25 30

Leu Gly Gly Leu Ile Leu Phe Gly Val Leu Gly Asn Ile Leu Val Ile
35 40 45

Leu Ser Val Ala Cys His Arg His Leu His Ser Val Thr His Tyr Tyr
50 55 60

Ile Val Asn Leu Ala Val Ala Asp Leu Leu Leu Thr Ser Thr Val Leu
65 70 75 80

Pro Phe Ser Ala Ile Phe Glu Val Leu Gly Tyr Trp Ala Phe Gly Arg
85 90 95

Val Phe Cys Asn Ile Trp Ala Ala Val Asp Val Leu Cys Cys Thr Ala
100 105 110

Ser Ile Met Gly Leu Cys Ile Ile Ser Ile Asp Arg Tyr Ile Gly Val
115 120 125

Ser Tyr Pro Leu Arg Tyr Pro Thr Ile Val Thr Gln Arg Arg Gly Leu
130 135 140

Met Ala Leu Leu Cys Val Trp Ala Leu Ser Leu Val Ile Ser Ile Gly
145 150 155 160

Pro Leu Phe Gly Trp Arg Gln Pro Ala Pro Glu Asp Glu Thr Ile Cys
165 170 175

Gln Ile Asn Glu Glu Pro Gly Tyr Val Leu Phe Ser Ala Leu Gly Ser
180 185 190

Phe Tyr Leu Pro Leu Ala Ile Ile Leu Val Met Tyr Cys Arg Val Tyr
195 200 205
Val Val Ala Lys Arg Glu Ser Arg Gly Leu Lys Ser Gly Leu Lys Thr
210 215 220
Asp Lys Ser Asp Ser Glu Gln Val Thr Leu Arg Ile His Arg Lys Asn
225 230 235 240
Ala Pro Ala Gly Gly Ser Gly Met Ala Ser Ala Lys Thr Lys Thr His
245 250 255
Phe Ser Val Arg Leu Leu Lys Phe Ser Arg Glu Lys Lys Ala Ala Lys
260 265 270
Thr Leu Gly Ile Val Val Gly Cys Phe Val Leu Cys Trp Leu Pro Phe
275 280 285
Phe Leu Val Met Pro Ile Gly Ser Phe Phe Pro Asp Phe Lys Pro Ser
290 295 300
Glu Thr Val Phe Lys Ile Val Phe Trp Leu Gly Tyr Leu Asn Ser Cys
305 310 315 320
Ile Asn Pro Ile Ile Tyr Pro Cys Ser Ser Gln Glu Phe Lys Lys Ala
325 330 335
Phe Gln Asn Val Leu Arg Ile Gln Cys Leu Arg Arg Lys Gln Ser Ser
340 345 350
Lys His Ala Leu Gly Tyr Thr Leu His Pro Pro Ser Gln Ala Val Glu
355 360 365
Gly Gln His Lys Asp Met Val Arg Ile Pro Val Gly Ser Arg Glu Thr
370 375 380
Phe Tyr Arg Ile Ser Lys Thr Asp Gly Val Cys Glu Trp Lys Phe Phe
385 390 395 400
Ser Ser Met Pro Arg Gly Ser Ala Arg Ile Thr Val Ser Lys Asp Gln
405 410 415
Ser Ser Cys Thr Thr Ala Arg Thr Lys Ser Arg Ser Val Thr Arg Leu
420 425 430
Glu Cys Ser Gly Met Ile Leu Ala His Cys Asn Leu Arg Leu Pro Gly
435 440 445

Ser Arg Asp Ser Pro Ala Ser Ala Ser Gln Ala Ala Gly Thr Thr Gly
 450 455 460

Asp Val Pro Pro Gly Arg Arg His Gln Ala Gln Leu Ile Phe Val Phe
 465 470 475 480

Leu Val Glu Thr Gly Phe His His Val Gly Gln Asp Asp Leu Asp Leu
 485 490 495

Leu Thr Ser

<210> 16

<211> 429

<212> PRT

<213> Homo sapiens

<400> 16

Met Val Phe Leu Ser Gly Asn Ala Ser Asp Ser Ser Asn Cys Thr Gln
 1 5 10 15

Pro Pro Ala Pro Val Asn Ile Ser Lys Ala Ile Leu Leu Gly Val Ile
 20 25 30

Leu Gly Gly Leu Ile Leu Phe Gly Val Leu Gly Asn Ile Leu Val Ile
 35 40 45

Leu Ser Val Ala Cys His Arg His Leu His Ser Val Thr His Tyr Tyr
 50 55 60

Ile Val Asn Leu Ala Val Ala Asp Leu Leu Leu Thr Ser Thr Val Leu
 65 70 75 80

Pro Phe Ser Ala Ile Phe Glu Val Leu Gly Tyr Trp Ala Phe Gly Arg
 85 90 95

Val Phe Cys Asn Ile Trp Ala Ala Val Asp Val Leu Cys Cys Thr Ala
 100 105 110

Ser Ile Met Gly Leu Cys Ile Ile Ser Ile Asp Arg Tyr Ile Gly Val
 115 120 125

Ser Tyr Pro Leu Arg Tyr Pro Thr Ile Val Thr Gln Arg Arg Gly Leu
 130 135 140

Met Ala Leu Leu Cys Val Trp Ala Leu Ser Leu Val Ile Ser Ile Gly

145		150		155		160									
Pro	Leu	Phe	Gly	Trp	Arg	Gln	Pro	Ala	Pro	Glu	Asp	Glu	Thr	Ile	Cys
			165					170						175	
Gln	Ile	Asn	Glu	Glu	Pro	Gly	Tyr	Val	Leu	Phe	Ser	Ala	Leu	Gly	Ser
		180					185						190		
Phe	Tyr	Leu	Pro	Leu	Ala	Ile	Ile	Leu	Val	Met	Tyr	Cys	Arg	Val	Tyr
	195						200					205			
Val	Val	Ala	Lys	Arg	Glu	Ser	Arg	Gly	Leu	Lys	Ser	Gly	Leu	Lys	Thr
	210					215					220				
Asp	Lys	Ser	Asp	Ser	Glu	Gln	Val	Thr	Leu	Arg	Ile	His	Arg	Lys	Asn
225					230					235					240
Ala	Pro	Ala	Gly	Gly	Ser	Gly	Met	Ala	Ser	Ala	Lys	Thr	Lys	Thr	His
			245						250					255	
Phe	Ser	Val	Arg	Leu	Leu	Lys	Phe	Ser	Arg	Glu	Lys	Lys	Ala	Ala	Lys
		260						265					270		
Thr	Leu	Gly	Ile	Val	Val	Gly	Cys	Phe	Val	Leu	Cys	Trp	Leu	Pro	Phe
	275						280					285			
Phe	Leu	Val	Met	Pro	Ile	Gly	Ser	Phe	Phe	Pro	Asp	Phe	Lys	Pro	Ser
	290					295					300				
Glu	Thr	Val	Phe	Lys	Ile	Val	Phe	Trp	Leu	Gly	Tyr	Leu	Asn	Ser	Cys
305					310					315					320
Ile	Asn	Pro	Ile	Ile	Tyr	Pro	Cys	Ser	Ser	Gln	Glu	Phe	Lys	Lys	Ala
			325						330					335	
Phe	Gln	Asn	Val	Leu	Arg	Ile	Gln	Cys	Leu	Arg	Arg	Lys	Gln	Ser	Ser
		340						345					350		
Lys	His	Ala	Leu	Gly	Tyr	Thr	Leu	His	Pro	Pro	Ser	Gln	Ala	Val	Glu
	355						360					365			
Gly	Gln	His	Lys	Asp	Met	Val	Arg	Ile	Pro	Val	Gly	Ser	Arg	Glu	Thr
	370					375					380				
Phe	Tyr	Arg	Ile	Ser	Lys	Thr	Asp	Gly	Val	Cys	Glu	Trp	Lys	Phe	Phe
385					390					395					400
Ser	Ser	Met	Pro	Arg	Gly	Ser	Ala	Arg	Ile	Thr	Val	Ser	Lys	Asp	Gln

405	410	415
Ser Ser Cys Thr Thr Ala Arg Gly His Thr Pro Met Thr		
420	425	
<210> 17		
<211> 455		
<212> PRT		
<213> Homo sapiens		
<400> 17		
Met Val Phe Leu Ser Gly Asn Ala Ser Asp Ser Ser Asn Cys Thr Gln		
1	5	10
15		
Pro Pro Ala Pro Val Asn Ile Ser Lys Ala Ile Leu Leu Gly Val Ile		
20	25	30
Leu Gly Gly Leu Ile Leu Phe Gly Val Leu Gly Asn Ile Leu Val Ile		
35	40	45
Leu Ser Val Ala Cys His Arg His Leu His Ser Val Thr His Tyr Tyr		
50	55	60
Ile Val Asn Leu Ala Val Ala Asp Leu Leu Leu Thr Ser Thr Val Leu		
65	70	75
80		
Pro Phe Ser Ala Ile Phe Glu Val Leu Gly Tyr Trp Ala Phe Gly Arg		
85	90	95
Val Phe Cys Asn Ile Trp Ala Ala Val Asp Val Leu Cys Cys Thr Ala		
100	105	110
Ser Ile Met Gly Leu Cys Ile Ile Ser Ile Asp Arg Tyr Ile Gly Val		
115	120	125
Ser Tyr Pro Leu Arg Tyr Pro Thr Ile Val Thr Gln Arg Arg Gly Leu		
130	135	140
Met Ala Leu Leu Cys Val Trp Ala Leu Ser Leu Val Ile Ser Ile Gly		
145	150	155
160		
Pro Leu Phe Gly Trp Arg Gln Pro Ala Pro Glu Asp Glu Thr Ile Cys		
165	170	175
Gln Ile Asn Glu Glu Pro Gly Tyr Val Leu Phe Ser Ala Leu Gly Ser		
180	185	190

Phe Tyr Leu Pro Leu Ala Ile Ile Leu Val Met Tyr Cys Arg Val Tyr			
195	200	205	
Val Val Ala Lys Arg Glu Ser Arg Gly Leu Lys Ser Gly Leu Lys Thr			
210	215	220	
Asp Lys Ser Asp Ser Glu Gln Val Thr Leu Arg Ile His Arg Lys Asn			
225	230	235	240
Ala Pro Ala Gly Gly Ser Gly Met Ala Ser Ala Lys Thr Lys Thr His			
	245	250	255
Phe Ser Val Arg Leu Leu Lys Phe Ser Arg Glu Lys Lys Ala Ala Lys			
	260	265	270
Thr Leu Gly Ile Val Val Gly Cys Phe Val Leu Cys Trp Leu Pro Phe			
	275	280	285
Phe Leu Val Met Pro Ile Gly Ser Phe Phe Pro Asp Phe Lys Pro Ser			
	290	295	300
Glu Thr Val Phe Lys Ile Val Phe Trp Leu Gly Tyr Leu Asn Ser Cys			
305	310	315	320
Ile Asn Pro Ile Ile Tyr Pro Cys Ser Ser Gln Glu Phe Lys Lys Ala			
	325	330	335
Phe Gln Asn Val Leu Arg Ile Gln Cys Leu Cys Arg Lys Gln Ser Ser			
	340	345	350
Lys His Ala Leu Gly Tyr Thr Leu His Pro Pro Ser Gln Ala Val Glu			
	355	360	365
Gly Gln His Lys Asp Met Val Arg Ile Pro Val Gly Ser Arg Glu Thr			
	370	375	380
Phe Tyr Arg Ile Ser Lys Thr Asp Gly Val Cys Glu Trp Lys Phe Phe			
385	390	395	400
Ser Ser Met Pro Arg Gly Ser Ala Arg Ile Thr Val Ser Lys Asp Gln			
	405	410	415
Ser Ser Cys Thr Thr Ala Arg Arg Gly Met Asp Cys Arg Tyr Phe Thr			
	420	425	430
Lys Asn Cys Arg Glu His Ile Lys His Val Asn Phe Met Met Pro Pro			
435	440	445	

Trp Arg Lys Gly Leu Glu Cys
 450 455

<210> 18

<211> 466

<212> PRT

<213> Rattus norvegicus

<400> 18

Met Val Leu Leu Ser Glu Asn Ala Ser Glu Gly Ser Asn Cys Thr His
 1 5 10 15

Pro Pro Ala Pro Val Asn Ile Ser Lys Ala Ile Leu Leu Gly Val Ile
 20 25 30

Leu Gly Gly Leu Ile Ile Phe Gly Val Leu Gly Asn Ile Leu Val Ile
 35 40 45

Leu Ser Val Ala Cys His Arg His Leu His Ser Val Thr His Tyr Tyr
 50 55 60

Ile Val Asn Leu Ala Val Ala Asp Leu Leu Leu Thr Ser Thr Val Leu
 65 70 75 80

Pro Phe Ser Ala Ile Phe Glu Ile Leu Gly Tyr Trp Ala Phe Gly Arg
 85 90 95

Val Phe Cys Asn Ile Trp Ala Ala Val Asp Val Leu Cys Cys Thr Ala
 100 105 110

Ser Ile Met Gly Leu Cys Ile Ile Ser Ile Asp Arg Tyr Ile Gly Val
 115 120 125

Ser Tyr Pro Leu Arg Tyr Pro Thr Ile Val Thr Gln Arg Arg Gly Val
 130 135 140

Arg Ala Leu Leu Cys Val Trp Val Leu Ser Leu Val Ile Ser Ile Gly
 145 150 155 160

Pro Leu Phe Gly Trp Arg Gln Pro Ala Pro Glu Asp Glu Thr Ile Cys
 165 170 175

Gln Ile Asn Glu Glu Pro Gly Tyr Val Leu Phe Ser Ala Leu Gly Ser
 180 185 190

Phe Tyr Val Pro Leu Ala Ile Ile Leu Val Met Tyr Cys Arg Val Tyr
 195 200 205

Val Val Ala Lys Arg Glu Ser Arg Gly Leu Lys Ser Gly Leu Lys Thr
210 215 220
Asp Lys Ser Asp Ser Glu Gln Val Thr Leu Arg Ile His Arg Lys Asn
225 230 235 240
Val Pro Ala Glu Gly Gly Gly Val Ser Ser Ala Lys Asn Lys Thr His
245 250 255
Phe Ser Val Arg Leu Leu Lys Phe Ser Arg Glu Lys Lys Ala Ala Lys
260 265 270
Thr Leu Gly Ile Val Val Gly Cys Phe Val Leu Cys Trp Leu Pro Phe
275 280 285
Phe Leu Val Met Pro Ile Gly Ser Phe Phe Pro Asp Phe Lys Pro Ser
290 295 300
Glu Thr Val Phe Lys Ile Val Phe Trp Leu Gly Tyr Leu Asn Ser Cys
305 310 315 320
Ile Asn Pro Ile Ile Tyr Pro Cys Ser Ser Gln Glu Phe Lys Lys Ala
325 330 335
Phe Gln Asn Val Leu Arg Ile Gln Cys Leu Arg Arg Arg Gln Ser Ser
340 345 350
Lys His Ala Leu Gly Tyr Thr Leu His Pro Pro Ser Gln Ala Leu Glu
355 360 365
Gly Gln His Arg Asp Met Val Arg Ile Pro Val Gly Ser Gly Glu Thr
370 375 380
Phe Tyr Lys Ile Ser Lys Thr Asp Gly Val Cys Glu Trp Lys Phe Phe
385 390 395 400
Ser Ser Met Pro Gln Gly Ser Ala Arg Ile Thr Val Pro Lys Asp Gln
405 410 415
Ser Ala Cys Thr Thr Ala Arg Val Arg Ser Lys Ser Phe Leu Gln Val
420 425 430
Cys Cys Cys Val Gly Ser Ser Ala Pro Arg Pro Glu Glu Asn His Gln
435 440 445
Val Pro Thr Ile Lys Ile His Thr Ile Ser Leu Gly Glu Asn Gly Glu
450 455 460

Glu Val
465

<210> 19
<211> 466
<212> PRT
<213> Mus musculus

<400> 19
Met Val Leu Leu Ser Glu Asn Ala Ser Glu Gly Ser Asn Cys Thr His
1 5 10 15
Pro Pro Ala Gln Val Asn Ile Ser Lys Ala Ile Leu Leu Gly Val Ile
20 25 30
Leu Gly Gly Leu Ile Ile Phe Gly Val Leu Gly Asn Ile Leu Val Ile
35 40 45
Leu Ser Val Ala Cys His Arg His Leu His Ser Val Thr His Tyr Tyr
50 55 60
Ile Val Asn Leu Ala Val Ala Asp Leu Leu Leu Thr Ser Thr Val Leu
65 70 75 80
Pro Phe Ser Ala Ile Phe Glu Ile Leu Gly Tyr Trp Ala Phe Gly Arg
85 90 95
Val Phe Cys Asn Ile Trp Ala Ala Val Asp Val Leu Cys Cys Thr Ala
100 105 110
Ser Ile Met Gly Leu Cys Ile Ile Ser Ile Asp Arg Tyr Ile Gly Val
115 120 125
Ser Tyr Pro Leu Arg Tyr Pro Thr Ile Val Thr Gln Arg Arg Gly Val
130 135 140
Arg Ala Leu Leu Cys Val Trp Ala Leu Ser Leu Val Ile Ser Ile Gly
145 150 155 160
Pro Leu Phe Gly Trp Arg Gln Gln Ala Pro Glu Asp Glu Thr Ile Cys
165 170 175
Gln Ile Asn Glu Glu Pro Gly Tyr Val Leu Phe Ser Ala Leu Gly Ser
180 185 190
Phe Tyr Val Pro Leu Thr Ile Ile Leu Val Met Tyr Cys Arg Val Tyr

195					200					205					
Val	Val	Ala	Lys	Arg	Glu	Ser	Arg	Gly	Leu	Lys	Ser	Gly	Leu	Lys	Thr
210					215					220					
Asp	Lys	Ser	Asp	Ser	Glu	Gln	Val	Thr	Leu	Arg	Ile	His	Arg	Lys	Asn
225					230					235					240
Val	Pro	Ala	Glu	Gly	Ser	Gly	Val	Ser	Ser	Ala	Lys	Asn	Lys	Thr	His
245					250					255					
Phe	Ser	Val	Arg	Leu	Leu	Lys	Phe	Ser	Arg	Glu	Lys	Lys	Ala	Ala	Lys
260					265					270					
Thr	Leu	Gly	Ile	Val	Val	Gly	Cys	Phe	Val	Leu	Cys	Trp	Leu	Pro	Phe
275					280					285					
Phe	Leu	Val	Met	Pro	Ile	Gly	Ser	Phe	Phe	Pro	Asn	Phe	Lys	Pro	Pro
290					295					300					
Glu	Thr	Val	Phe	Lys	Ile	Val	Phe	Trp	Leu	Gly	Tyr	Leu	Asn	Ser	Cys
305					310					315					320
Ile	Asn	Pro	Ile	Ile	Tyr	Pro	Cys	Ser	Ser	Gln	Glu	Phe	Lys	Lys	Ala
325					330					335					
Phe	Gln	Asn	Val	Leu	Arg	Ile	Gln	Cys	Leu	Arg	Arg	Arg	Gln	Ser	Ser
340					345					350					
Lys	His	Ala	Leu	Gly	Tyr	Thr	Leu	His	Pro	Pro	Ser	Gln	Ala	Val	Glu
355					360					365					
Glu	Gln	His	Arg	Gly	Met	Val	Arg	Ile	Pro	Val	Gly	Ser	Gly	Glu	Thr
370					375					380					
Phe	Tyr	Lys	Ile	Ser	Lys	Thr	Asp	Gly	Val	Cys	Glu	Trp	Lys	Phe	Phe
385					390					395					400
Ser	Ser	Met	Pro	Gln	Gly	Ser	Ala	Arg	Ile	Thr	Met	Pro	Lys	Asp	Gln
405					410					415					
Ser	Ala	Cys	Thr	Thr	Ala	Arg	Val	Arg	Ser	Lys	Ser	Phe	Leu	Gln	Val
420					425					430					
Cys	Cys	Cys	Val	Gly	Ser	Ser	Thr	Pro	Arg	Pro	Glu	Glu	Asn	His	Gln
435					440					445					
Val	Pro	Thr	Ile	Lys	Ile	His	Thr	Ile	Ser	Leu	Gly	Glu	Asn	Gly	Glu

450 455 460
 Glu Val
 465

 <210> 20
 <211> 466
 <212> PRT
 <213> Bos taurus

 <400> 20
 Met Val Phe Leu Ser Gly Asn Ala Ser Asp Ser Ser Asn Cys Thr His
 1 5 10 15
 Pro Pro Pro Pro Val Asn Ile Ser Lys Ala Ile Leu Leu Gly Val Ile
 20 25 30
 Leu Gly Gly Leu Ile Leu Phe Gly Val Leu Gly Asn Ile Leu Val Ile
 35 40 45
 Leu Ser Val Ala Cys His Arg His Leu His Ser Val Thr His Tyr Tyr
 50 55 60
 Ile Val Asn Leu Ala Val Ala Asp Leu Leu Leu Thr Ser Thr Val Leu
 65 70 75 80
 Pro Phe Ser Ala Ile Phe Glu Ile Leu Gly Tyr Trp Ala Phe Gly Arg
 85 90 95
 Val Phe Cys Asn Val Trp Ala Ala Val Asp Val Leu Cys Cys Thr Ala
 100 105 110
 Ser Ile Met Gly Leu Cys Ile Ile Ser Ile Asp Arg Tyr Ile Gly Val
 115 120 125
 Ser Tyr Pro Leu Arg Tyr Pro Thr Ile Val Thr Gln Lys Arg Gly Leu
 130 135 140
 Met Ala Leu Leu Cys Val Trp Ala Leu Ser Leu Val Ile Ser Ile Gly
 145 150 155 160
 Pro Leu Phe Gly Trp Arg Gln Pro Ala Pro Glu Asp Glu Thr Ile Cys
 165 170 175
 Gln Ile Asn Glu Glu Pro Gly Tyr Val Leu Phe Ser Ala Leu Gly Ser
 180 185 190

Phe Tyr Val Pro Leu Thr Ile Ile Leu Val Met Tyr Cys Arg Val Tyr			
195	200	205	
Val Val Ala Lys Arg Glu Ser Arg Gly Leu Lys Ser Gly Leu Lys Thr			
210	215	220	
Asp Lys Ser Asp Ser Glu Gln Val Thr Leu Arg Ile His Arg Lys Asn			
225	230	235	240
Ala Gln Val Gly Gly Ser Gly Val Thr Ser Ala Lys Asn Lys Thr His			
	245	250	255
Phe Ser Val Arg Leu Leu Lys Phe Ser Arg Glu Lys Lys Ala Ala Lys			
	260	265	270
Thr Leu Gly Ile Val Val Gly Cys Phe Val Leu Cys Trp Leu Pro Phe			
	275	280	285
Phe Leu Val Met Pro Ile Gly Ser Phe Phe Pro Asp Phe Arg Pro Ser			
	290	295	300
Glu Thr Val Phe Lys Ile Ala Phe Trp Leu Gly Tyr Leu Asn Ser Cys			
305	310	315	320
Ile Asn Pro Ile Ile Tyr Pro Cys Ser Ser Gln Glu Phe Lys Lys Ala			
	325	330	335
Phe Gln Asn Val Leu Arg Ile Gln Cys Leu Arg Arg Lys Gln Ser Ser			
	340	345	350
Lys His Thr Leu Gly Tyr Thr Leu His Ala Pro Ser His Val Leu Glu			
	355	360	365
Gly Gln His Lys Asp Leu Val Arg Ile Pro Val Gly Ser Ala Glu Thr			
	370	375	380
Phe Tyr Lys Ile Ser Lys Thr Asp Gly Val Cys Glu Trp Lys Ile Phe			
385	390	395	400
Ser Ser Leu Pro Arg Gly Ser Ala Arg Met Ala Val Ala Arg Asp Pro			
	405	410	415
Ser Ala Cys Thr Thr Ala Arg Val Arg Ser Lys Ser Phe Leu Gln Val			
	420	425	430
Cys Cys Cys Leu Gly Pro Ser Thr Pro Ser His Gly Glu Asn His Gln			
435	440	445	

Ile Pro Thr Ile Lys Ile His Thr Ile Ser Leu Ser Glu Asn Gly Glu
 450 455 460

Glu Val
 465

<210> 21
 <211> 295
 <212> PRT
 <213> Canis familiaris

<400> 21
 Met Val Phe Leu Ser Gly Asn Ala Ser Asp Ser Ser Asn Cys Thr His
 1 5 10 15

Pro Pro Ala Pro Val Asn Ile Ser Lys Ala Ile Leu Leu Gly Val Ile
 20 25 30

Leu Gly Gly Leu Ile Ile Phe Gly Val Leu Gly Asn Ile Leu Val Ile
 35 40 45

Leu Ser Val Ala Cys His Arg His Leu His Ser Val Thr His Tyr Tyr
 50 55 60

Ile Val Asn Leu Ala Val Ala Asp Leu Leu Leu Thr Ser Thr Val Leu
 65 70 75 80

Pro Phe Ser Ala Ile Phe Glu Ile Leu Gly Tyr Trp Ala Phe Gly Arg
 85 90 95

Val Phe Cys Asn Ile Trp Ala Ala Val Asp Val Leu Cys Cys Thr Ala
 100 105 110

Ser Ile Met Gly Leu Cys Ile Ile Ser Ile Asp Arg Tyr Ile Gly Val
 115 120 125

Ser Tyr Pro Leu Arg Tyr Pro Thr Ile Val Thr Gln Lys Arg Gly Leu
 130 135 140

Met Ala Leu Leu Cys Val Trp Ala Leu Ser Leu Val Ile Ser Ile Gly
 145 150 155 160

Pro Leu Phe Gly Trp Arg Gln Pro Ala Pro Glu Asp Glu Thr Ile Cys
 165 170 175

Gln Ile Thr Glu Glu Pro Gly Tyr Val Leu Phe Ser Ala Leu Gly Ser
 180 185 190

Phe Tyr Val Pro Leu Thr Ile Ile Leu Val Met Tyr Cys Arg Val Tyr
 195 200 205

Val Val Ala Lys Arg Glu Ser Arg Gly Leu Lys Ser Gly Leu Lys Thr
 210 215 220

Asp Lys Ser Asp Ser Glu Gln Val Thr Leu Arg Ile His Arg Lys Asn
 225 230 235 240

Ala Pro Val Gly Gly Thr Gly Val Ser Ser Ala Lys Asn Lys Thr His
 245 250 255

Phe Ser Val Arg Leu Leu Lys Phe Ser Arg Glu Lys Lys Ala Ala Lys
 260 265 270

Thr Leu Gly Ile Val Val Gly Cys Phe Val Leu Cys Trp Leu Pro Phe
 275 280 285

Phe Leu Val Met Pro Ile Gly
 290 295

<210> 22
 <211> 466
 <212> PRT
 <213> Oryctolagus cuniculus

<400> 22
 Met Val Phe Leu Ser Gly Asn Ala Ser Asp Ser Ser Asn Cys Thr His
 1 5 10 15

Pro Pro Ala Pro Val Asn Ile Ser Lys Ala Ile Leu Leu Gly Val Ile
 20 25 30

Leu Gly Gly Leu Ile Leu Phe Gly Val Leu Gly Asn Ile Leu Val Ile
 35 40 45

Leu Ser Val Ala Cys His Arg His Leu His Ser Val Thr His Tyr Tyr
 50 55 60

Ile Val Asn Leu Ala Val Ala Asp Leu Leu Leu Thr Ser Thr Val Leu
 65 70 75 80

Pro Phe Ser Ala Ile Phe Glu Ile Leu Gly Tyr Trp Ala Phe Gly Arg
 85 90 95

Val Phe Cys Asn Ile Trp Ala Ala Val Asp Val Leu Cys Cys Thr Ala

100	105	110
Ser Ile Ile Ser Leu Cys Val Ile Ser Ile Asp Arg Tyr Ile Gly Val		
115	120	125
Ser Tyr Pro Leu Arg Tyr Pro Thr Ile Val Thr Gln Arg Arg Gly Leu		
130	135	140
Arg Ala Leu Leu Cys Val Trp Ala Phe Ser Leu Val Ile Ser Val Gly		
145	150	155 160
Pro Leu Phe Gly Trp Arg Gln Pro Ala Pro Asp Asp Glu Thr Ile Cys		
	165	170 175
Gln Ile Asn Glu Glu Pro Gly Tyr Val Leu Phe Ser Ala Leu Gly Ser		
	180	185 190
Phe Tyr Val Pro Leu Thr Ile Ile Leu Ala Met Tyr Cys Arg Val Tyr		
	195	200 205
Val Val Ala Lys Arg Glu Ser Arg Gly Leu Lys Ser Gly Leu Lys Thr		
	210	215 220
Asp Lys Ser Asp Ser Glu Gln Val Thr Leu Arg Ile His Arg Lys Asn		
225	230	235 240
Ala Pro Ala Gly Gly Ser Gly Val Ala Ser Ala Lys Asn Lys Thr His		
	245	250 255
Phe Ser Val Arg Leu Leu Lys Phe Ser Arg Glu Lys Lys Ala Ala Lys		
	260	265 270
Thr Leu Gly Ile Val Val Gly Cys Phe Val Leu Cys Trp Leu Pro Phe		
	275	280 285
Phe Leu Val Met Pro Ile Gly Ser Phe Phe Pro Asp Phe Lys Pro Pro		
	290	295 300
Glu Thr Val Phe Lys Ile Val Phe Trp Leu Gly Tyr Leu Asn Ser Cys		
305	310	315 320
Ile Asn Pro Ile Ile Tyr Pro Cys Ser Ser Gln Glu Phe Lys Lys Ala		
	325	330 335
Phe Gln Asn Val Leu Lys Ile Gln Cys Leu Arg Arg Lys Gln Ser Ser		
	340	345 350
Lys His Ala Leu Gly Tyr Thr Leu His Ala Pro Ser Gln Ala Leu Glu		

355 360 365
 Gly Gln His Lys Asp Met Val Arg Ile Pro Val Gly Ser Gly Glu Thr
 370 375 380
 Phe Tyr Lys Ile Ser Lys Thr Asp Gly Val Cys Glu Trp Lys Phe Phe
 385 390 395 400
 Ser Ser Met Pro Arg Gly Ser Ala Arg Ile Thr Val Pro Lys Asp Gln
 405 410 415
 Ser Ala Cys Thr Thr Ala Arg Val Arg Ser Lys Ser Phe Leu Gln Val
 420 425 430
 Cys Cys Cys Val Gly Pro Ser Thr Pro Asn Pro Gly Glu Asn His Gln
 435 440 445
 Val Pro Thr Ile Lys Ile His Thr Ile Ser Leu Ser Glu Asn Gly Glu
 450 455 460
 Glu Val
 465
 <210> 23
 <211> 466
 <212> PRT
 <213> Homo sapiens
 <400> 23
 Met Val Phe Leu Ser Gly Asn Ala Ser Asp Ser Ser Asn Cys Thr Gln
 1 5 10 15
 Pro Pro Ala Pro Val Asn Ile Ser Lys Ala Ile Leu Leu Gly Val Ile
 20 25 30
 Leu Gly Gly Leu Ile Leu Phe Gly Val Leu Gly Asn Ile Leu Val Ile
 35 40 45
 Leu Ser Val Ala Cys His Arg His Leu His Ser Val Thr His Tyr Tyr
 50 55 60
 Ile Val Asn Leu Ala Val Ala Asp Leu Leu Leu Thr Ser Thr Val Leu
 65 70 75 80
 Pro Phe Ser Ala Ile Phe Glu Val Leu Gly Tyr Trp Ala Phe Gly Arg
 85 90 95

Val	Phe	Cys	Asn	Ile	Trp	Ala	Ala	Val	Asp	Val	Leu	Cys	Cys	Thr	Ala	100	105	110
Ser	Ile	Met	Gly	Leu	Cys	Ile	Ile	Ser	Ile	Asp	Arg	Tyr	Ile	Gly	Val	115	120	125
Ser	Tyr	Pro	Leu	Arg	Tyr	Pro	Thr	Ile	Val	Thr	Gln	Arg	Arg	Gly	Leu	130	135	140
Met	Ala	Leu	Leu	Cys	Val	Trp	Ala	Leu	Ser	Leu	Val	Ile	Ser	Ile	Gly	145	150	155
Pro	Leu	Phe	Gly	Trp	Arg	Gln	Pro	Ala	Pro	Glu	Asp	Glu	Thr	Ile	Cys	165	170	175
Gln	Ile	Asn	Glu	Glu	Pro	Gly	Tyr	Val	Leu	Phe	Ser	Ala	Leu	Gly	Ser	180	185	190
Phe	Tyr	Leu	Pro	Leu	Ala	Ile	Ile	Leu	Val	Met	Tyr	Cys	Arg	Val	Tyr	195	200	205
Val	Val	Ala	Lys	Arg	Glu	Ser	Arg	Gly	Leu	Lys	Ser	Gly	Leu	Lys	Thr	210	215	220
Asp	Lys	Ser	Asp	Ser	Glu	Gln	Val	Thr	Leu	Arg	Ile	His	Arg	Lys	Asn	225	230	235
Ala	Pro	Ala	Gly	Gly	Ser	Gly	Met	Ala	Ser	Ala	Lys	Thr	Lys	Thr	His	245	250	255
Phe	Ser	Val	Arg	Leu	Leu	Lys	Phe	Ser	Arg	Glu	Lys	Lys	Ala	Ala	Lys	260	265	270
Thr	Leu	Gly	Ile	Val	Val	Gly	Cys	Phe	Val	Leu	Cys	Trp	Leu	Pro	Phe	275	280	285
Phe	Leu	Val	Met	Pro	Ile	Gly	Ser	Phe	Phe	Pro	Asp	Phe	Lys	Pro	Ser	290	295	300
Glu	Thr	Val	Phe	Lys	Ile	Val	Phe	Trp	Leu	Gly	Tyr	Leu	Asn	Ser	Cys	305	310	315
Ile	Asn	Pro	Ile	Ile	Tyr	Pro	Cys	Ser	Ser	Gln	Glu	Phe	Lys	Lys	Ala	325	330	335
Phe	Gln	Asn	Val	Leu	Arg	Ile	Gln	Cys	Leu	Cys	Arg	Lys	Gln	Ser	Ser	340	345	350

Lys His Ala Leu Gly Tyr Thr Leu His Pro Pro Ser Gln Ala Val Glu
 355 360 365

Gly Gln His Lys Asp Met Val Arg Ile Pro Val Gly Ser Arg Glu Thr
 370 375 380

Phe Tyr Arg Ile Ser Lys Thr Asp Gly Val Cys Glu Trp Lys Phe Phe
 385 390 395 400

Ser Ser Met Pro Arg Gly Ser Ala Arg Ile Thr Val Ser Lys Asp Gln
 405 410 415

Ser Ser Cys Thr Thr Ala Arg Val Arg Ser Lys Ser Phe Leu Gln Val
 420 425 430

Cys Cys Cys Val Gly Pro Ser Thr Pro Ser Leu Asp Lys Asn His Gln
 435 440 445

Val Pro Thr Ile Lys Val His Thr Ile Ser Leu Ser Glu Asn Gly Glu
 450 455 460

Glu Val
 465

<210> 24
 <211> 470
 <212> PRT
 <213> *Oryzias latipes*

<400> 24
 Met Thr Pro Ser Ser Val Thr Leu Asn Cys Ser Asn Cys Ser His Val
 1 5 10 15

Leu Ala Pro Glu Leu Asn Thr Val Lys Ala Val Val Leu Gly Met Val
 20 25 30

Leu Gly Ile Phe Ile Leu Phe Gly Val Ile Gly Asn Ile Leu Val Ile
 35 40 45

Leu Ser Val Val Cys His Arg His Leu Gln Thr Val Thr Tyr Tyr Phe
 50 55 60

Ile Val Asn Leu Ala Val Ala Asp Leu Leu Leu Ser Ser Thr Val Leu
 65 70 75 80

Pro Phe Ser Ala Ile Phe Glu Ile Leu Asp Arg Trp Val Phe Gly Arg
 85 90 95

Val Phe Cys Asn Ile Trp Ala Ala Val Asp Val Leu Cys Cys Thr Ala	100	105	110
Ser Ile Met Ser Leu Cys Val Ile Ser Val Asp Arg Tyr Ile Gly Val	115	120	125
Ser Tyr Pro Leu Arg Tyr Pro Ala Ile Met Thr Lys Arg Arg Ala Leu	130	135	140
Leu Ala Val Met Leu Leu Trp Val Leu Ser Val Ile Ile Ser Ile Gly	145	150	155 160
Pro Leu Phe Gly Trp Lys Glu Pro Ala Pro Glu Asp Glu Thr Val Cys	165	170	175
Lys Ile Thr Glu Glu Pro Gly Tyr Ala Ile Phe Ser Ala Val Gly Ser	180	185	190
Phe Tyr Leu Pro Leu Ala Ile Ile Leu Ala Met Tyr Cys Arg Val Tyr	195	200	205
Val Val Ala Gln Lys Glu Ser Arg Gly Leu Lys Glu Gly Gln Lys Ile	210	215	220
Glu Lys Ser Asp Ser Glu Gln Val Ile Leu Arg Met His Arg Gly Asn	225	230	235 240
Thr Thr Val Ser Glu Asp Glu Ala Leu Arg Ser Arg Thr His Phe Ala	245	250	255
Leu Arg Leu Leu Lys Phe Ser Arg Glu Lys Lys Ala Ala Lys Thr Leu	260	265	270
Gly Ile Val Val Gly Cys Phe Val Leu Cys Trp Leu Pro Phe Phe Leu	275	280	285
Val Leu Pro Ile Gly Ser Ile Phe Pro Ala Tyr Arg Pro Ser Asp Thr	290	295	300
Val Phe Lys Ile Thr Phe Trp Leu Gly Tyr Phe Asn Ser Cys Ile Asn	305	310	315 320
Pro Ile Ile Tyr Leu Cys Ser Asn Gln Glu Phe Lys Lys Ala Phe Gln	325	330	335
Ser Leu Leu Gly Val His Cys Leu Arg Met Thr Pro Arg Ala His His	340	345	350

His His Leu Ser Val Gly Gln Ser Gln Thr Gln Gly His Ser Leu Thr
 355 360 365

Ile Ser Leu Asp Ser Lys Gly Ala Pro Cys Arg Leu Ser Pro Ser Ser
 370 375 380

Ser Val Ala Leu Ser Arg Thr Pro Ser Ser Arg Asp Ser Arg Glu Trp
 385 390 395 400

Arg Val Phe Ser Gly Gly Pro Ile Asn Ser Gly Pro Gly Pro Thr Glu
 405 410 415

Ala Gly Arg Ala Lys Val Ala Lys Leu Cys Asn Lys Ser Leu His Arg
 420 425 430

Thr Cys Cys Cys Ile Leu Arg Ala Arg Thr Pro Thr Gln Asp Pro Ala
 435 440 445

Pro Leu Gly Asp Leu Pro Thr Ile Lys Ile His Gln Leu Ser Leu Ser
 450 455 460

Glu Lys Gly Glu Ser Val
 465 470

<210> 25
 <211> 391
 <212> PRT
 <213> Branchiostoma lanceolatum

<400> 25
 Met Ser Ala Asn Thr Thr Val Ser Pro Thr Glu Thr Thr Ala Asn Leu
 1 5 10 15

Thr Ala Asn Ser Thr Glu Ala Ser Val Gly Ser Cys Phe Ala Pro Asn
 20 25 30

Pro Tyr Ser Ala Gly Val Gln Ala Val Leu Gly Leu Ile Thr Val Ile
 35 40 45

Leu Ile Leu Leu Thr Val Ile Gly Asn Val Leu Val Ile Leu Ala Val
 50 55 60

Thr Cys His Arg Lys Met Arg Thr Val Thr Asn Phe Phe Ile Val Ser
 65 70 75 80

Leu Ala Cys Ala Asp Leu Ser Val Gly Ile Thr Val Leu Pro Phe Ala

				85				90				95			
Ala	Thr	Asn	Asp	Ile	Leu	Gly	Tyr	Trp	Pro	Phe	Gly	Gly	Tyr	Cys	Asp
100				105				110							
Val	Trp	Val	Ser	Phe	Asp	Val	Leu	Asn	Ser	Thr	Ala	Ser	Ile	Leu	Asn
115				120				125							
Leu	Val	Val	Ile	Ala	Phe	Asp	Arg	Phe	Leu	Ala	Ile	Thr	Ala	Pro	Phe
130				135				140							
Thr	Tyr	His	Thr	Arg	Met	Thr	Glu	Arg	Thr	Ala	Gly	Ile	Leu	Ile	Ala
145				150				155				160			
Thr	Val	Trp	Gly	Ile	Ser	Leu	Val	Val	Ser	Phe	Leu	Pro	Ile	Gln	Ala
165				170				175							
Gly	Trp	Tyr	Arg	Asp	Asn	Gln	Ser	Glu	Glu	Ala	Leu	Ala	Ile	Tyr	Ser
180				185				190							
Asp	Pro	Cys	Leu	Cys	Ile	Phe	Thr	Ala	Ser	Thr	Ala	Tyr	Thr	Ile	Val
195				200				205							
Ser	Ser	Leu	Ile	Ser	Phe	Tyr	Ile	Pro	Leu	Leu	Ile	Met	Leu	Val	Phe
210				215				220							
Tyr	Gly	Ile	Ile	Phe	Lys	Ala	Ala	Arg	Asp	Gln	Ala	Arg	Lys	Ile	Asn
225				230				235				240			
Ala	Leu	Glu	Gly	Arg	Leu	Glu	Gln	Glu	Asn	Asn	Arg	Gly	Lys	Lys	Ile
245				250				255							
Ser	Leu	Ala	Lys	Glu	Lys	Lys	Ala	Ala	Lys	Thr	Leu	Gly	Ile	Ile	Met
260				265				270							
Gly	Val	Phe	Ile	Leu	Cys	Trp	Leu	Pro	Phe	Phe	Val	Val	Asn	Ile	Val
275				280				285							
Asn	Pro	Phe	Cys	Asp	Arg	Cys	Val	Gln	Pro	Ala	Val	Phe	Ile	Ala	Leu
290				295				300							
Thr	Trp	Leu	Gly	Trp	Ile	Asn	Ser	Cys	Phe	Asn	Pro	Ile	Ile	Tyr	Ala
305				310				315				320			
Phe	Asn	Lys	Glu	Phe	Arg	Lys	Val	Phe	Val	Lys	Met	Ile	Cys	Cys	His
325				330				335							
Lys	Cys	Arg	Gly	Val	Thr	Val	Gly	Pro	Asn	His	Ala	Asp	Leu	Asn	Tyr

340 345 350
 Asp Pro Val Ala Met Arg Leu Lys Lys Arg Gly Glu Asn Ala Asn Gly
 355 360 365
 Thr Val Asn Gly Asp Ala Asn Gly Lys Ala Asn Gly Asn Ile Glu Ala
 370 375 380
 Gly Glu Gly Thr Ser Ser Ser
 385 390

<210> 26
 <211> 36
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthesized
 peptide

<400> 26
 Met Thr Ser Thr Cys Thr Asn Ser Thr Arg Glu Ser Asn Ser Ser His
 1 5 10 15
 Thr Cys Met Pro Leu Ser Lys Met Pro Ile Ser Leu Ala His Gly Ile
 20 25 30
 Ile Arg Ser Thr
 35

<210> 27
 <211> 13
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthesized
 peptide

<400> 27
 Gln Arg Lys Pro Gln Leu Leu Gln Val Thr Asn Arg Phe
 1 5 10

<210> 28
 <211> 5

<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthesized
peptide

<400> 28
Trp Pro Leu Asn Ser
1 5

<210> 29
<211> 20
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthesized
peptide

<400> 29
Asp Arg Tyr Leu Ser Ile Ile His Pro Leu Ser Tyr Pro Ser Lys Met
1 5 10 15

Thr Gln Arg Arg
20

<210> 30
<211> 23
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthesized
peptide

<400> 30
Gly Gln Ala Ala Phe Asp Glu Arg Asn Ala Leu Cys Ser Met Ile Trp
1 5 10 15

Gly Ala Ser Pro Ser Tyr Thr
20

<210> 31
<211> 182

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthesized peptide

<400> 31

Cys Ala Ala Arg Arg Gln His Ala Leu Leu Tyr Asn Val Lys Arg His
1 5 10 15

Ser Leu Glu Val Arg Val Lys Asp Cys Val Glu Asn Glu Asp Glu Glu
20 25 30

Gly Ala Glu Lys Lys Glu Glu Phe Gln Asp Glu Ser Glu Phe Arg Arg
35 40 45

Gln His Glu Gly Glu Val Lys Ala Lys Glu Gly Arg Met Glu Ala Lys
50 55 60

Asp Gly Ser Leu Lys Ala Lys Glu Gly Ser Thr Gly Thr Ser Glu Ser
65 70 75 80

Ser Val Glu Ala Gly Ser Glu Glu Val Arg Glu Ser Ser Thr Val Ala
85 90 95

Ser Asp Gly Ser Met Glu Gly Lys Glu Gly Ser Thr Lys Val Glu Glu
100 105 110

Asn Ser Met Lys Ala Asp Lys Gly Arg Thr Glu Val Asn Gln Cys Ser
115 120 125

Ile Asp Leu Gly Glu Asp Asp Met Glu Phe Gly Glu Asp Asp Ile Asn
130 135 140

Phe Ser Glu Asp Asp Val Glu Ala Val Asn Ile Pro Glu Ser Leu Pro
145 150 155 160

Pro Ser Arg Arg Asn Ser Asn Ser Asn Pro Pro Leu Pro Arg Cys Tyr
165 170 175

Gln Cys Lys Ala Ala Lys
180

<210> 32

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthesized peptide

<400> 32

Ala Val Leu Ala Val Trp Val Asp Val Glu Thr Gln Val Pro Gln
1 5 10 15

<210> 33

<211> 55

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthesized peptide

<400> 33

Tyr Gly Tyr Met His Lys Thr Ile Lys Lys Glu Ile Gln Asp Met Leu
1 5 10 15

Lys Lys Phe Phe Cys Lys Glu Lys Pro Pro Lys Glu Asp Ser His Pro
20 25 30

Asp Leu Pro Gly Thr Glu Gly Gly Thr Glu Gly Lys Ile Val Pro Ser
35 40 45

Tyr Asp Ser Ala Thr Phe Pro
50 55

<210> 34

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: HGPRBMY8 sense primer

<400> 34

gcagagcact cctccactct

20

<210> 35

<211> 20
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: HGPRBMY8
anti-sense primer

<400> 35
agcaggcaat catgacaatc

20

<210> 36
<211> 20
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: GPCR84 sense
primer

<400> 36
gttagcctca cccacctgtt

20

<210> 37
<211> 20
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: GPCR84
anti-sense primer

<400> 37
cacaatccag gtgcataga

20

<210> 38
<211> 42
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: HGPRBMY8 5'
primer

<400> 38

gtccccaagc ttgcaccatg acgtccacct gcaccaacag ca

42

<210> 39

<211> 62

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: HGPRBMY8 3'

Flag-tag primer

<400> 39

cgggataccta cttgtcgtcg tcgtccttgt agtccatagg aaaagtagca gaatcgtagg 60
aa 62

<210> 40

<211> 407

<212> PRT

<213> Homo sapiens

<400> 40

Met Ser Leu Asn Ser Ser Leu Ser Cys Arg Lys Glu Leu Ser Asn Leu
1 5 10 15

Thr Glu Glu Glu Gly Gly Glu Gly Gly Val Ile Ile Thr Gln Phe Ile
20 25 30

Ala Ile Ile Val Ile Thr Ile Phe Val Cys Leu Gly Asn Leu Val Ile
35 40 45

Val Val Thr Leu Tyr Lys Lys Ser Tyr Leu Leu Thr Leu Ser Asn Lys
50 55 60

Phe Val Phe Ser Leu Thr Leu Ser Asn Phe Leu Leu Ser Val Leu Val
65 70 75 80

Leu Pro Phe Val Val Thr Ser Ser Ile Arg Arg Glu Trp Ile Phe Gly
85 90 95

Val Val Trp Cys Asn Phe Ser Ala Leu Leu Tyr Leu Leu Ile Ser Ser
100 105 110

Ala Ser Met Leu Thr Leu Gly Val Ile Ala Ile Asp Arg Tyr Tyr Ala
115 120 125

Val Leu Tyr Pro Met Val Tyr Pro Met Lys Ile Thr Gly Asn Arg Ala

130		135		140
Val Met Ala Leu Val Tyr Ile Trp Leu His Ser Leu Ile Gly Cys Leu				
145		150		155 160
Pro Pro Leu Phe Gly Trp Ser Ser Val Glu Phe Asp Glu Phe Lys Trp				
	165		170	175
Met Cys Val Ala Ala Trp His Arg Glu Pro Gly Tyr Thr Ala Phe Trp				
	180		185	190
Gln Ile Trp Cys Ala Leu Phe Pro Phe Leu Val Met Leu Val Cys Tyr				
	195		200	205
Gly Phe Ile Phe Arg Val Ala Arg Val Lys Ala Arg Lys Val His Cys				
	210		215	220
Gly Thr Val Val Ile Val Glu Glu Asp Ala Gln Arg Thr Gly Arg Lys				
	225		230 235	240
Asn Ser Ser Thr Ser Thr Ser Ser Ser Gly Ser Arg Arg Asn Ala Phe				
	245		250	255
Gln Gly Val Val Tyr Ser Ala Asn Gln Cys Lys Ala Leu Ile Thr Ile				
	260		265	270
Leu Val Val Leu Gly Ala Phe Met Val Thr Trp Gly Pro Tyr Met Val				
	275		280	285
Val Ile Ala Ser Glu Ala Leu Trp Gly Lys Ser Ser Val Ser Pro Ser				
	290		295	300
Leu Glu Thr Trp Ala Thr Trp Leu Ser Phe Ala Ser Ala Val Cys His				
	305		310 315	320
Pro Leu Ile Tyr Gly Leu Trp Asn Lys Thr Val Arg Lys Glu Leu Leu				
	325		330	335
Gly Met Cys Phe Gly Asp Arg Tyr Tyr Arg Glu Pro Phe Val Gln Arg				
	340		345	350
Gln Arg Thr Ser Arg Leu Phe Ser Ile Ser Asn Arg Ile Thr Asp Leu				
	355		360	365
Gly Leu Ser Pro His Leu Thr Ala Leu Met Ala Gly Gly Gln Pro Leu				
	370		375	380
Gly His Ser Ser Ser Thr Gly Asp Thr Gly Phe Ser Cys Ser Gln Asp				

385 390 395 400
 Ser Gly Asn Leu Arg Ala Leu
 405

 <210> 41
 <211> 448
 <212> PRT
 <213> Homo sapiens

 <400> 41
 Met Thr Ser Thr Cys Thr Asn Ser Thr Arg Glu Ser Asn Ser Ser His
 1 5 10 15

 Thr Cys Met Pro Leu Ser Lys Met Pro Ile Ser Leu Ala His Gly Ile
 20 25 30

 Ile Arg Ser Thr Val Leu Val Ile Phe Leu Ala Ala Ser Phe Val Gly
 35 40 45

 Asn Ile Val Leu Ala Leu Val Leu Gln Arg Lys Pro Gln Leu Leu Gln
 50 55 60

 Val Thr Asn Arg Phe Ile Phe Asn Leu Leu Val Thr Asp Leu Leu Gln
 65 70 75 80

 Ile Ser Leu Val Ala Pro Trp Val Val Ala Thr Ser Val Pro Leu Phe
 85 90 95

 Trp Pro Leu Asn Ser His Phe Cys Thr Ala Leu Val Ser Leu Thr His
 100 105 110

 Leu Phe Ala Phe Ala Ser Val Asn Thr Ile Val Val Val Ser Val Asp
 115 120 125

 Arg Tyr Leu Ser Ile Ile His Pro Leu Ser Tyr Pro Ser Lys Met Thr
 130 135 140

 Gln Arg Arg Gly Tyr Leu Leu Leu Tyr Gly Thr Trp Ile Val Ala Ile
 145 150 155 160

 Leu Gln Ser Thr Pro Pro Leu Tyr Gly Trp Gly Gln Ala Ala Phe Asp
 165 170 175

 Glu Arg Asn Ala Leu Cys Ser Met Ile Trp Gly Ala Ser Pro Ser Tyr
 180 185 190

Thr	Ile	Leu	Ser	Val	Val	Ser	Phe	Ile	Val	Ile	Pro	Leu	Ile	Val	Met	195	200	205	
Ile	Ala	Cys	Tyr	Ser	Val	Val	Phe	Cys	Ala	Ala	Arg	Arg	Gln	His	Ala	210	215	220	
Leu	Leu	Tyr	Asn	Val	Lys	Arg	His	Ser	Leu	Glu	Val	Arg	Val	Lys	Asp	225	230	235	240
Cys	Val	Glu	Asn	Glu	Asp	Glu	Glu	Gly	Ala	Glu	Lys	Lys	Glu	Glu	Phe	245	250	255	
Gln	Asp	Glu	Ser	Glu	Phe	Arg	Arg	Gln	His	Glu	Gly	Glu	Val	Lys	Ala	260	265	270	
Lys	Glu	Gly	Arg	Met	Glu	Ala	Lys	Asp	Gly	Ser	Leu	Lys	Ala	Lys	Glu	275	280	285	
Gly	Ser	Thr	Gly	Thr	Ser	Glu	Ser	Ser	Val	Glu	Ala	Arg	Gly	Ser	Glu	290	295	300	
Glu	Val	Arg	Glu	Ser	Ser	Thr	Val	Ala	Ser	Asp	Gly	Ser	Met	Glu	Gly	305	310	315	320
Lys	Glu	Gly	Ser	Thr	Lys	Val	Glu	Glu	Asn	Ser	Met	Lys	Ala	Asp	Lys	325	330	335	
Gly	Arg	Thr	Glu	Val	Asn	Gln	Cys	Ser	Ile	Asp	Leu	Gly	Glu	Asp	Asp	340	345	350	
Met	Glu	Phe	Gly	Glu	Asp	Asp	Ile	Asn	Phe	Ser	Glu	Asp	Asp	Val	Glu	355	360	365	
Ala	Val	Asn	Ile	Pro	Glu	Ser	Leu	Pro	Pro	Ser	Arg	Arg	Asn	Ser	Asn	370	375	380	
Ser	Asn	Pro	Pro	Leu	Pro	Arg	Cys	Tyr	Gln	Cys	Lys	Ala	Lys	Lys	Val	385	390	395	400
Ile	Phe	Ile	Ile	Ile	Phe	Ser	Tyr	Val	Leu	Ser	Leu	Gly	Pro	Tyr	Cys	405	410	415	
Phe	Leu	Ala	Val	Glu	Asp	Ser	His	Pro	Asp	Leu	Pro	Gly	Thr	Glu	Gly	420	425	430	
Gly	Thr	Glu	Gly	Lys	Ile	Val	Pro	Ser	Tyr	Asp	Ser	Ala	Thr	Phe	Pro	435	440	445	

<210> 42

<211> 448

<212> PRT

<213> Homo sapiens

<400> 42

Met	Thr	Ser	Thr	Cys	Thr	Asn	Ser	Thr	Arg	Glu	Ser	Asn	Ser	Ser	His
1				5					10					15	

Thr	Cys	Met	Pro	Leu	Ser	Lys	Met	Pro	Ile	Ser	Leu	Ala	His	Gly	Ile
			20					25					30		

Ile	Arg	Ser	Thr	Val	Leu	Val	Ile	Phe	Leu	Ala	Ala	Ser	Phe	Val	Gly
	35						40					45			

Asn	Ile	Val	Leu	Ala	Leu	Val	Leu	Gln	Arg	Lys	Pro	Gln	Leu	Leu	Gln
	50					55					60				

Val	Thr	Asn	Arg	Phe	Ile	Phe	Asn	Leu	Leu	Val	Thr	Asp	Leu	Leu	Gln
65					70					75					80

Ile	Ser	Leu	Val	Ala	Pro	Trp	Val	Val	Ala	Thr	Ser	Val	Pro	Leu	Phe
				85					90					95	

Trp	Pro	Leu	Asn	Ser	His	Phe	Cys	Thr	Ala	Leu	Val	Ser	Leu	Thr	His
			100					105					110		

Leu	Phe	Ala	Phe	Ala	Ser	Val	Asn	Thr	Ile	Val	Val	Val	Ser	Val	Asp
	115						120					125			

Arg	Tyr	Leu	Ser	Ile	Ile	His	Pro	Leu	Ser	Tyr	Pro	Ser	Lys	Met	Thr
	130					135					140				

Gln	Arg	Arg	Gly	Tyr	Leu	Leu	Leu	Tyr	Gly	Thr	Trp	Ile	Val	Ala	Ile
145					150					155					160

Leu	Gln	Ser	Thr	Pro	Pro	Leu	Tyr	Gly	Trp	Gly	Gln	Ala	Ala	Phe	Asp
				165					170					175	

Glu	Arg	Asn	Ala	Leu	Cys	Ser	Met	Ile	Trp	Gly	Ala	Ser	Pro	Ser	Tyr
			180					185					190		

Thr	Ile	Leu	Ser	Val	Val	Ser	Phe	Ile	Val	Ile	Pro	Leu	Ile	Val	Met
		195					200					205			

Ile Ala Cys Tyr Ser Val Val Phe Cys Ala Ala Arg Arg Gln His Ala
 210 215 220

Leu Leu Tyr Asn Val Lys Arg His Ser Leu Glu Val Arg Val Lys Asp
 225 230 235 240

Cys Val Glu Asn Glu Asp Glu Glu Gly Ala Glu Lys Lys Glu Glu Phe
 245 250 255

Gln Asp Glu Ser Glu Phe Arg Arg Gln His Glu Gly Glu Val Lys Ala
 260 265 270

Lys Glu Gly Arg Met Glu Ala Lys Asp Gly Ser Leu Lys Ala Lys Glu
 275 280 285

Gly Ser Thr Gly Thr Ser Glu Ser Ser Val Glu Ala Arg Gly Ser Glu
 290 295 300

Glu Val Arg Glu Ser Ser Thr Val Ala Ser Asp Gly Ser Met Glu Gly
 305 310 315 320

Lys Glu Gly Ser Thr Lys Val Glu Glu Asn Ser Met Lys Ala Asp Lys
 325 330 335

Gly Arg Thr Glu Val Asn Gln Cys Ser Ile Asp Leu Gly Glu Asp Asp
 340 345 350

Met Glu Phe Gly Glu Asp Asp Ile Asn Phe Ser Glu Asp Asp Val Glu
 355 360 365

Ala Val Asn Ile Pro Glu Ser Leu Pro Pro Ser Arg Arg Asn Ser Asn
 370 375 380

Ser Asn Pro Pro Leu Pro Arg Cys Tyr Gln Cys Lys Ala Lys Lys Val
 385 390 395 400

Ile Phe Ile Ile Ile Phe Ser Tyr Val Leu Ser Leu Gly Pro Tyr Cys
 405 410 415

Phe Leu Ala Val Glu Asp Ser His Pro Asp Leu Pro Gly Thr Glu Gly
 420 425 430

Gly Thr Glu Gly Lys Ile Val Pro Ser Tyr Asp Ser Ala Thr Phe Pro
 435 440 445

<210> 43

<211> 448

<212> PRT

<213> Homo sapiens

<400> 43

Met Thr Ser Thr Cys Thr Asn Ser Thr Arg Glu Ser Asn Ser Ser His
1 5 10 15

Thr Cys Met Pro Leu Ser Lys Met Pro Ile Ser Leu Ala His Gly Ile
20 25 30

Ile Arg Ser Thr Val Leu Val Ile Phe Leu Ala Ala Ser Phe Val Gly
35 40 45

Asn Ile Val Leu Ala Leu Val Leu Gln Arg Lys Pro Gln Leu Leu Gln
50 55 60

Val Thr Asn Arg Phe Ile Phe Asn Leu Leu Val Thr Asp Leu Leu Gln
65 70 75 80

Ile Ser Leu Val Ala Pro Trp Val Val Ala Thr Ser Val Pro Leu Phe
85 90 95

Trp Pro Leu Asn Ser His Phe Cys Thr Ala Leu Val Ser Leu Thr His
100 105 110

Leu Phe Ala Phe Ala Ser Val Asn Thr Ile Val Leu Val Ser Val Asp
115 120 125

Arg Tyr Leu Ser Ile Ile His Pro Leu Ser Tyr Pro Ser Lys Met Thr
130 135 140

Gln Arg Arg Gly Tyr Leu Leu Leu Tyr Gly Thr Trp Ile Val Ala Ile
145 150 155 160

Leu Gln Ser Thr Pro Pro Leu Tyr Gly Trp Gly Gln Ala Ala Phe Asp
165 170 175

Glu Arg Asn Ala Leu Cys Ser Met Ile Trp Gly Ala Ser Pro Ser Tyr
180 185 190

Thr Ile Leu Ser Val Val Ser Phe Ile Val Ile Pro Leu Ile Val Met
195 200 205

Ile Ala Cys Tyr Ser Val Val Phe Cys Ala Ala Arg Arg Gln His Ala

210	215	220
Leu Leu Tyr Asn Val Lys Arg His Ser Leu Glu Val Arg Val Lys Asp		
225	230	235 240
Cys Val Glu Asn Glu Asp Glu Glu Gly Ala Glu Lys Lys Glu Glu Phe		
	245	250 255
Gln Asp Glu Ser Glu Phe Arg Arg Gln His Glu Gly Glu Val Lys Ala		
	260	265 270
Lys Glu Gly Arg Met Glu Ala Lys Asp Gly Ser Leu Lys Ala Lys Glu		
	275	280 285
Gly Ser Thr Gly Thr Ser Glu Ser Ser Val Glu Ala Arg Gly Ser Glu		
	290	295 300
Glu Val Arg Glu Ser Ser Thr Val Ala Ser Asp Gly Ser Met Glu Gly		
305	310	315 320
Lys Glu Gly Ser Thr Lys Val Glu Glu Asn Ser Met Lys Ala Asp Lys		
	325	330 335
Gly Arg Thr Glu Val Asn Gln Cys Ser Ile Asp Leu Gly Glu Asp Gly		
	340	345 350
Met Glu Phe Gly Glu Asp Asp Ile Asn Phe Ser Glu Asp Asp Val Glu		
	355	360 365
Ala Val Asn Ile Pro Glu Ser Leu Pro Pro Ser Arg Arg Asn Ser Asn		
	370	375 380
Ser Asn Pro Pro Leu Pro Arg Cys Tyr Gln Cys Lys Ala Ala Lys Val		
385	390	395 400
Ile Phe Ile Ile Ile Phe Ser Tyr Val Leu Ser Leu Gly Pro Tyr Cys		
	405	410 415
Phe Leu Ala Val Glu Asp Ser His Pro Asp Leu Pro Gly Thr Glu Gly		
	420	425 430
Gly Thr Glu Gly Lys Ile Val Pro Ser Tyr Asp Ser Ala Thr Phe Pro		
	435	440 445

<210> 44
 <211> 1659
 <212> DNA
 <213> Homo sapiens

<400> 44
 gcctgcaacc tgtcycacgc cctctggctg ttgccatgac gtccacctgc accaacagca 60
 cgcgcgagag taacagcagc cacacgtgca tgcccctctc caaaatgccc atcagcctgg 120
 cccacggcat catccgctca accgtgctgg ttatcttctc cgccgcctct ttcgtcggca 180
 acatagtgtc ggcgctagt ttgcagcgca agccgcagct gctgcaggtg accaaccgtt 240
 ttatctttta cctcctcgtc accgacctgc tgcagatttc gctcgtggcc ccctgggtgg 300
 tggccacctc tgtgcctctc ttctggcccc tcaacagcca cttctgcacg gccctggtta 360
 gcctcaccga cctgttcgcc ttcgccagcg tcaacaccat tgtcttggtg tcagtggatc 420
 gctacttgtc catcatccac cctctctcct acccgctcaa gatgacctag cgccgcgggt 480
 acctgctcct ctatggcacc tggattgtgg ccacctgca gagcactcct ccactctacg 540
 gctggggcca ggctgccttt gatgagcgca atgctctctg ctccatgatc tggggggcca 600
 gccccagcta cactattctc agcgtggtgt ccttcatcgt cattccactg attgtcatga 660
 ttgectgcta ctccgtggtg ttctgtgcag cccggaggca gcatgctctg ctgtacaatg 720
 tcaagagaca cagcttgga gtgcgagtca aggactgtgt ggagaatgag gatgaagagg 780
 gagcagagaa gaaggaggag ttccaggatg agagtgagtt tcgccgccag catgaagggtg 840
 aggtcaaggc caaggagggc agaatggaag ccaaggacgg cagcctgaag gccaaggaag 900
 gaagcacggg gaccagttag agtagttag aggccagggg cagcgaggag gtcagagaga 960
 gcagcacggg ggccagcgac ggcagcatgg agggtaagga aggcagcacc aaagttgagg 1020
 agaacagcat gaaggcagac aagggtcgca cagaggtaaa ccagtgcagc attgacttgg 1080
 gtgaagatgg catggagttt ggtgaagacg acatcaattt cagtgaggat gacgtcgagg 1140
 cagtgaacat cccggagagc ctcccaccca gtcgtcgtaa cagcaacagc aacctctctc 1200
 tgcccagggtg ctaccagtgc aaagctgcta aagtgatctt catcatcatt ttctcctatg 1260
 tgctatccct ggggccctac tgcttttttag cagtcctggc cgtgtgggtg gatgtcgaaa 1320
 cccaggtagc ccagtgggtg atcaccataa tcatctggct tttcttctctg cagtgtctga 1380
 tccaccctta tgtctatggc tacatgcaca agaccattaa gaaggaaatc caggacatgc 1440
 tgaagaagtt cttctgcaag gaaaagcccc cgaaagaaga tagccacca gacctgccc 1500
 gaacagaggg tgggactgaa ggcaagattg tcccttctta cgattctgct acttttctct 1560
 gaagtttagt ctaaggcaaa ccttgaaaat cagtccttca gccacagcta ttagagctt 1620
 taaaactacc aggttcaatc actggttatg ctttctgtg 1659

<210> 45
 <211> 1527
 <212> DNA
 <213> Homo sapiens

<400> 45
 atgacgtcca cctgcaccaa cagcacgcgc gagagtaaca gcagccacac gtgcatgccc 60
 ctctccaaaa tgcccatcag cctggcccac ggcacatcc gctcaaccgt gctgggttatc 120
 ttctctgccc cctctttctg cggcaacata gtgctggcgc tagtggtgca gcgcaagccg 180
 cagctgctgc aggtgaccaa ccgtttttatc tttaacctcc tcgtcacga cctgctgcag 240
 atttctgctg tggccccctg ggtggtggcc acctctgtgc ctctcttctg gccctcaac 300
 agccacttct gcacggccct ggttagcctc accacactgt tcgccttcgc cagcgtcaac 360

accattgtcg	tggtgtcagt	ggatcgctac	ttgtccatca	tccacctct	ctcctaccg	420
tccaagatga	cccagcgccg	cggttacctg	ctcctctatg	gcacctggat	tgtggccatc	480
ctgcagagca	ctcctccact	ctacggctgg	ggccaggctg	cctttgatga	gcgcaatgct	540
ctctgtcca	tgatctgggg	ggccagcccc	agctacacta	ttctcagcgt	ggtgtccttc	600
atcgtcattc	cactgattgt	catgattgcc	tgctactccg	tggtgttctg	tgcagcccg	660
aggcagcatg	ctctgctgta	caatgtcaag	agacacagct	tggaagtgcg	agtcaaggac	720
tgtgtggaga	atgaggatga	agaggagca	gagaagaagg	aggagttcca	ggatgagagt	780
gagtttcgcc	gccagcatga	aggtgaggtc	aaggccaagg	agggcagaat	ggaagccaag	840
gacggcagcc	tgaaggccaa	ggaaggaagc	acggggacca	gtgagagtag	tgtagaggcc	900
aggggcagcg	aggaggtcag	agagagcagc	acggtggcca	gcgacggcag	catggagggg	960
aaggaaggca	gcaccaaagt	tgaggagaac	agcatgaagg	cagacaaggg	tcgcacagag	1020
gtcaaccagt	gcagcattga	cttgggtgaa	gatgacatgg	agtttggtga	agacgacatc	1080
aatttcagtg	aggatgacgt	cgaggcagtg	aacatcccgg	agagcctccc	accagtcgt	1140
cgtaacagca	acagcaaccc	tcctctgccc	aggtgctacc	agtgcaaagc	tgctaaagtg	1200
atcttcatca	tcattttctc	ctatgtgcta	tccttggggc	cctactgctt	tttagcagtc	1260
ctggccgtgt	gggtggatgt	cgaaaccag	gtacccagct	gggtgatcac	cataatcatc	1320
tggtttttct	tcctgcagtg	ctgcatccac	ccctatgtct	atggctacat	gcacaagacc	1380
attaagaagg	aaatccagga	catgctgaag	aagttcttct	gcaaggaaaa	gccccgaaa	1440
gaagatagcc	accagacct	gcccgaaca	gaggggtggga	ctgaaggcaa	gattgtccct	1500
tcctacgatt	ctgctacttt	tccttga				1527

<210> 46

<211> 1527

<212> DNA

<213> Homo sapiens

<400> 46

atgacgtcca	cctgcaccaa	cagcacgcgc	gagagtaaca	gcagccacac	gtgcatgccc	60
ctctccaaaa	tgcccatcag	cctggcccac	ggcatcatcc	gctcaaccgt	gctgggttatc	120
ttcctcgccg	cctctttcgt	cggcaacata	gtgctggcgc	tagtgttgca	gcgcaagccg	180
cagctgctgc	aggtgaccaa	ccgttttata	tttaacctcc	tcgtcaccga	cctgctgcag	240
atttcgctcg	tggccccctg	ggtgggtggc	acctctgtgc	ctctcttctg	gcccccaac	300
agccacttct	gcacggccct	ggttagcctc	accacactgt	tcgccttcgc	cagcgtcaac	360
accattgtcg	tggtgtcagt	ggatcgctac	ttgtccatca	tccacctct	ctcctaccg	420
tccaagatga	cccagcgccg	cggttacctg	ctcctctatg	gcacctggat	tgtggccatc	480
ctgcagagca	ctcctccact	ctacggctgg	ggccaggctg	cctttgatga	gcgcaatgct	540
ctctgtcca	tgatctgggg	ggccagcccc	agctacacta	ttctcagcgt	ggtgtccttc	600
atcgtcattc	cactgattgt	catgattgcc	tgctactccg	tggtgttctg	tgcagcccg	660
aggcagcatg	ctctgctgta	caatgtcaag	agacacagct	tggaagtgcg	agtcaaggac	720
tgtgtggaga	atgaggatga	agaggagca	gagaagaagg	aggagttcca	ggatgagagt	780
gagtttcgcc	gccagcatga	aggtgaggtc	aaggccaagg	agggcagaat	ggaagccaag	840
gacggcagcc	tgaaggccaa	ggaaggaagc	acggggacca	gtgagagtag	tgtagaggcc	900
aggggcagcg	aggaggtcag	agagagcagc	acggtggcca	gcgacggcag	catggagggg	960
aaggaaggca	gcaccaaagt	tgaggagaac	agcatgaagg	cagacaaggg	tcgcacagag	1020
gtcaaccagt	gcagcattga	cttgggtgaa	gatgacatgg	agtttggtga	agacgacatc	1080
aatttcagtg	aggatgacgt	cgaggcagtg	aacatcccgg	agagcctccc	accagtcgt	1140
cgtaacagca	acagcaaccc	tcctctgccc	aggtgctacc	agtgcaaagc	taagaaagtg	1200

atcttcatca	tcattttctc	ctatgtgcta	tccctggggc	cctactgctt	tttagcagtc	1260
ctggccgtgt	gggtggatgt	cgaaacccag	gtaccccagt	gggtgatcac	cataatcatc	1320
tggtttttct	tctgacagt	ctgcatccac	ccctatgtct	atggctacat	gcacaagacc	1380
attaagaagg	aatccagga	catgctgaag	aagttcttct	gcaaggaaaa	gccccgaaa	1440
gaagatagcc	accagacct	gcccggaaca	gaggggtggga	ctgaaggcaa	gattgtccct	1500
tcctacgatt	ctgctacttt	tccttga				1527

<210> 47

<211> 1580

<212> DNA

<213> Homo sapiens

<400> 47

gcaacctgtc	tcacgccctc	tggtgtttgc	catgacgtcc	acctgcacca	acagcacgcg	60
cgagagtaac	agcagccaca	cgtgcatgcc	cctctccaaa	atgcccatca	gcctggccca	120
cggcatcatc	cgtcaaccg	tgctggttat	cttctctgcc	gcctctttcg	tcggcaacat	180
agtgtgtggc	ctagtgttgc	agcgcaagcc	gcagctgctg	caggtgacca	accgttttat	240
ctttaacctc	ctcgtcaccg	acctgctgca	gatttcgctc	gtggccccct	gggtgggtggc	300
cacctctgtg	cctctcttct	ggccccctca	cagccacttc	tgcacggccc	tggttagcct	360
caccacactg	ttcgccttcg	ccagcgtcaa	caccattgtc	ttggtgtcag	tggtatcgcta	420
cttgtccatc	atccaccctc	tctcctaccc	gtccaagatg	accagcgcgc	gcggttacct	480
gctcctctat	ggcacctgga	ttgtggccat	cctgcagagc	actcctccac	tctacggctg	540
gggccaggct	gcctttgatg	agcgcaatgc	tctctgctcc	atgatctggg	gggccagccc	600
cagctacact	attctcagcg	tggtgtcctt	catcgtcatt	ccactgattg	tcattgattgc	660
ctgctactcc	gtggtgttct	gtgcagcccg	gaggcagcat	gctctgctgt	acaatgtcaa	720
gagacacagc	ttggaagtgc	gagtcaagga	ctgtgtggag	aatgaggatg	aagagggagc	780
agagaagaag	gaggagtcc	aggatgagag	tgagtttcgc	cgccagcatg	aaggtgaggt	840
caaggccaag	gagggcagaa	tggaagccaa	ggacggcagc	ctgaaggcca	aggaaggaag	900
cacggggacc	agtgtgagta	gtgttagaggc	caggggcagc	gaggaggtca	gagagagcag	960
cacgggtggc	agcgacggca	gcatggaggg	taagggaaggc	agcaccaaag	ttgaggagaa	1020
cagcatgaag	gcagacaagg	gtcgcacaga	ggtcaaccag	tgcagcattg	acttgggtga	1080
agatgacatg	gagtttggtg	aagacgacat	caatttcagt	gaggatgacg	tcgaggcagt	1140
gaacatcccc	gagagcctcc	caccagtcg	tcgtaacagc	aacagcaacc	ctcctctgcc	1200
caggtgctac	cagtgcacaa	ctgctaaagt	gatcttcac	atcattttct	cctatgtgct	1260
atccctgggg	ccctactgct	tttttagcag	cctggccgtg	tggttggtg	tcgaaaccca	1320
ggtaccccc	tggttgatca	ccataatcat	ctggcttttc	ttcctgcagt	gctgcatcca	1380
cccctatgtc	tatggctaca	tgcaacaagc	cattaagaag	gaaatccagg	acatgctgaa	1440
gaagttcttc	tgcaaggaaa	agcccccgaa	agaagatagc	caccagacc	tgccccgaac	1500
agaggggtgg	actgaaggca	agattgtccc	ttcctacgat	tctgctactt	ttccttgaag	1560
ttagttctaa	ggcaaacctt					1580

<210> 48

<211> 1527

<212> DNA

<213> Homo sapiens

<220>
 <221> modified_base
 <222> (1192)..(1194)
 <223> n=a or t or g or c

<400> 48
 atgacgtcca cctgcaccaa cagcacgcgc gagagtaaca gcagccacac gtgcatgccc 60
 ctctccaaaa tgcccatcag cctggcccac ggcatcatcc gctcaaccgt gctgggttattc 120
 ttctctgcgc cctcttttcgt cggcaacata gtgctggcgc tagtggttgca gcgcaagccg 180
 cagctgctgc aggtgaccaa ccgtttttatc tttaacctcc tcgtcaccga cctgctgcag 240
 atttcgctcg tggcccccctg ggtgggtggcc acctctgtgc ctctctttctg gcccttcaac 300
 agccactttct gcacggccct ggtagcctc acccactgt tcgccttcgc cagcgtcaac 360
 accattgten tgggtgtcagt ggatcgctac ttgtccatca tccaccctct ctctaccgcg 420
 tccaagatga cccagcgccg cggttacctg ctctcttatg gcacctggat tgtggccatc 480
 ctgcagagca ctctccact ctacggctgg gccaggtcg cctttgatga gcgcaatgct 540
 ctctgctcca tgatctgggg ggccagcccc agctacacta ttctcagcgt ggtgtccttc 600
 atcgtcattc cactgattgt catgattgcc tgctactccg tgggtgttctg tgcagcccg 660
 aggcagcatg ctctgctgta caatgtcaag agacacagct tggagtgcg agtcaaggac 720
 tgtgtggaga atgaggatga agaggagca gagaagaagg aggagttcca ggatgagagt 780
 gagtttctgcc gccagcatga aggtgaggtc aaggccaagg agggcagaat ggaagccaag 840
 gacggcagcc tgaaggccaa ggaaggaagc acggggacca gtgagagtag tgtagaggcc 900
 aggggcagcg aggaggtcag agagagcagc acggtggcca gcgacggcag catggagggt 960
 aaggaaggca gcaccaaagt tgaggagaac agcatgaagg cagacaaggg tcgcacagag 1020
 gtcaaccagt gcagcattga cttgggtgaa gatgncatgg agtttggtga agacgacatc 1080
 aatttcagtg aggatgacgt cgaggcagtg aacatcccgg agagcctccc acccagtcgt 1140
 cgtaacagca acagcaaccc tcctctgccc aggtgctacc agtgcaaagc tnnnaaagtg 1200
 atcttcatca tcattttctc ctatgtgcta tccctggggc cctactgctt tttagcagtc 1260
 ctggccgtgt ggggtggatgt cgaaaccag gtacccaggt ggggtgatcac cataatcatc 1320
 tggcttttct tcctgcagtg ctgcatccac ccctatgtct atggctacat gcacaagacc 1380
 attaagaagg aaatccagga catgctgaag aagttcttct gcaaggaaaa gccccgaaa 1440
 gaagatagcc acccagacct gcccggaaca gaggggtggga ctgaaggcaa gattgtccct 1500
 tcctacgatt ctgctacttt tccttga 1527

<210> 49
 <211> 508
 <212> PRT
 <213> Homo sapiens

<220>
 <221> VARIANT
 <222> (124)
 <223> Xaa=Unknown, modified, or any amino acid

<220>
 <221> VARIANT
 <222> (398)
 <223> Xaa=Unknown, modified, or any amino acid

<400> 49

Met	Thr	Ser	Thr	Cys	Thr	Asn	Ser	Thr	Arg	Glu	Ser	Asn	Ser	Ser	His
1				5					10					15	
Thr	Cys	Met	Pro	Leu	Ser	Lys	Met	Pro	Ile	Ser	Leu	Ala	His	Gly	Ile
			20					25					30		
Ile	Arg	Ser	Thr	Val	Leu	Val	Ile	Phe	Leu	Ala	Ala	Ser	Phe	Val	Gly
		35					40					45			
Asn	Ile	Val	Leu	Ala	Leu	Val	Leu	Gln	Arg	Lys	Pro	Gln	Leu	Leu	Gln
	50					55					60				
Val	Thr	Asn	Arg	Phe	Ile	Phe	Asn	Leu	Leu	Val	Thr	Asp	Leu	Leu	Gln
65					70					75				80	
Ile	Ser	Leu	Val	Ala	Pro	Trp	Val	Val	Ala	Thr	Ser	Val	Pro	Leu	Phe
				85					90					95	
Trp	Pro	Leu	Asn	Ser	His	Phe	Cys	Thr	Ala	Leu	Val	Ser	Leu	Thr	His
			100					105					110		
Leu	Phe	Ala	Phe	Ala	Ser	Val	Asn	Thr	Ile	Val	Xaa	Val	Ser	Val	Asp
	115						120					125			
Arg	Tyr	Leu	Ser	Ile	Ile	His	Pro	Leu	Ser	Tyr	Pro	Ser	Lys	Met	Thr
	130					135					140				
Gln	Arg	Arg	Gly	Tyr	Leu	Leu	Leu	Tyr	Gly	Thr	Trp	Ile	Val	Ala	Ile
145					150					155				160	
Leu	Gln	Ser	Thr	Pro	Pro	Leu	Tyr	Gly	Trp	Gly	Gln	Ala	Ala	Phe	Asp
				165					170					175	
Glu	Arg	Asn	Ala	Leu	Cys	Ser	Met	Ile	Trp	Gly	Ala	Ser	Pro	Ser	Tyr
		180						185					190		
Thr	Ile	Leu	Ser	Val	Val	Ser	Phe	Ile	Val	Ile	Pro	Leu	Ile	Val	Met
		195					200					205			
Ile	Ala	Cys	Tyr	Ser	Val	Val	Phe	Cys	Ala	Ala	Arg	Arg	Gln	His	Ala
	210						215				220				
Leu	Leu	Tyr	Asn	Val	Lys	Arg	His	Ser	Leu	Glu	Val	Arg	Val	Lys	Asp
225					230					235				240	
Cys	Val	Glu	Asn	Glu	Asp	Glu	Glu	Gly	Ala	Glu	Lys	Lys	Glu	Glu	Phe

	245		250		255
Gln Asp Glu Ser Glu Phe Arg Arg Gln His Glu Gly Glu Val Lys Ala					
	260		265		270
Lys Glu Gly Arg Met Glu Ala Lys Asp Gly Ser Leu Lys Ala Lys Glu					
	275		280		285
Gly Ser Thr Gly Thr Ser Glu Ser Ser Val Glu Ala Arg Gly Ser Glu					
	290		295		300
Glu Val Arg Glu Ser Ser Thr Val Ala Ser Asp Gly Ser Met Glu Gly					
305		310		315	320
Lys Glu Gly Ser Thr Lys Val Glu Glu Asn Ser Met Lys Ala Asp Lys					
	325		330		335
Gly Arg Thr Glu Val Asn Gln Cys Ser Ile Asp Leu Gly Glu Asp Xaa					
	340		345		350
Met Glu Phe Gly Glu Asp Asp Ile Asn Phe Ser Glu Asp Asp Val Glu					
	355		360		365
Ala Val Asn Ile Pro Glu Ser Leu Pro Pro Ser Arg Arg Asn Ser Asn					
	370		375		380
Ser Asn Pro Pro Leu Pro Arg Cys Tyr Gln Cys Lys Ala Xaa Lys Val					
385		390		395	400
Ile Phe Ile Ile Ile Phe Ser Tyr Val Leu Ser Leu Gly Pro Tyr Cys					
	405		410		415
Phe Leu Ala Val Leu Ala Val Trp Val Asp Val Glu Thr Gln Val Pro					
	420		425		430
Gln Trp Val Ile Thr Ile Ile Ile Trp Leu Phe Phe Leu Gln Cys Cys					
	435		440		445
Ile His Pro Tyr Val Tyr Gly Tyr Met His Lys Thr Ile Lys Lys Glu					
	450		455		460
Ile Gln Asp Met Leu Lys Lys Phe Phe Cys Lys Glu Lys Pro Pro Lys					
465		470		475	480
Glu Asp Ser His Pro Asp Leu Pro Gly Thr Glu Gly Gly Thr Glu Gly					
	485		490		495
Lys Ile Val Pro Ser Tyr Asp Ser Ala Thr Phe Pro					

<210> 50
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: SNP

<400> 50
caccattgtc ttggtgtcag t 21

<210> 51
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: SNP

<400> 51
caccattgtc gtggtgtcag t 21

<210> 52
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: SNP

<400> 52
ggtgaagatg acatggagtt t 21

<210> 53
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: SNP

<400> 53

ggtgaagatg gcatggagtt t 21

<210> 54
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: SNP

<400> 54
gtgcaaagct gctaaagtga t 21

<210> 55
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: SNP

<400> 55
gtgcaaagct actaaagtga t 21

<210> 56
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: SNP

<400> 56
tgcaaagctg ctaaagtgat c 21

<210> 57
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: SNP

<400> 57

tgcaaagctg ataaagtgat c

21

<210> 58

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: SNP

<400> 58

gcaaagctgc taaagtgatc t

21

<210> 59

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: SNP

<400> 59

gcaaagctgc gaaagtgatc t

21

<210> 60

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: GAPDH F3
Forward primer

<400> 60

agccgagcca catcgct

17

<210> 61

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: GAPDH R1
Reverse primer

<400> 61
 gtgaccaggc gcccaatac 19

<210> 62
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: GAPDH-PVIC
 Taqman(R) Probe

<400> 62
 caaatccgtt gactccgacc ttcacctt 28

<210> 63
 <211> 99
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 Oligonucleotide 1

<220>
 <221> modified_base
 <222> (25)..(84)
 <223> n=a+g+c+t and b=c+g+t

<400> 63
 cgaagcgtaa gggcccagcc ggccnnbnnb nnbnnbnnbn nbnnbnnbnn bnnbnnbnnb 60
 nnbnnbnnbn nbnnbnnbnn bnnbccgggt ccgggcggc 99

<210> 64
 <211> 95
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 Oligonucleotide 2N=A+G+C+T and V=C+A+G

<220>
 <221> modified_base

<222> (21)..(80)

<223> n=a or g or c or t; v=c or a or g

<400> 64

aaaaggaaaa aagcggccgc vnnvnnvnnv nnvnnvnnvn nvnnvnnvnn vnnvnnvnnv 60
nnvnnvnnvn nvnnvnnvnn gccgcccga cccgg 95

<210> 65

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 65

Pro Gly Pro Gly Gly
1 5

<210> 66

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 66

Gly Asp Phe Trp Tyr Glu Ala Cys Glu Ser Ser Cys Ala Phe Trp
1 5 10 15

<210> 67

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 67

Leu Glu Trp Gly Ser Asp Val Phe Tyr Asp Val Tyr Asp Cys Cys
1 5 10 15

<210> 68
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 68
Cys Leu Arg Ser Gly Thr Gly Cys Ala Phe Gln Leu Tyr Arg Phe
1 5 10 15

<210> 69
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 69
Asn Asn Phe Pro Cys Leu Arg Ser Gly Arg Asn Cys Asp Ala Gly
1 5 10 15

<210> 70
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 70
Arg Ile Val Pro Asn Gly Tyr Phe Asn Val His Gly Arg Ser Leu
1 5 10 15

<210> 71
<211> 14
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 71

Arg Ile Asp Ser Cys Ala Lys Tyr Phe Leu Arg Ser Cys Asp
1 5 10

<210> 72

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic 5' primer

<400> 72

gcagcagcgg ccgcaccgtg ctgggttatct tcctcgccg

39

<210> 73

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic 3' primer

<400> 73

gcagcagtcg acaggaaaag tagcagaatc gtagg

35

<210> 74

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic 5' primer

<400> 74

gcagcagcgg ccgcatgacg tccacctgca ccaacagc

38

<210> 75
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic 3'
primer

<400> 75
gcagcagtcg acatagacat aggggtggat gcagcac

37

<210> 76
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 76
Ser Thr Cys Thr Asn Ser Thr Arg Glu Ser Asn Ser Ser
1 5 10

<210> 77
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 77
Gln Leu Leu Gln Val Thr Asn Arg Phe Ile Phe Asn Leu
1 5 10

<210> 78
<211> 13
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 78

Tyr Pro Ser Lys Met Thr Gln Arg Arg Gly Tyr Leu Leu
1 5 10

<210> 79

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 79

Glu Ala Lys Asp Gly Ser Leu Lys Ala Lys Glu Gly Ser
1 5 10

<210> 80

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 80

Glu Gly Lys Glu Gly Ser Thr Lys Val Glu Glu Asn Ser
1 5 10

<210> 81

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 81

Lys Val Glu Glu Asn Ser Met Lys Ala Asp Lys Gly Arg
1 5 10

<210> 82
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 82
Glu Ser Leu Pro Pro Ser Arg Arg Asn Ser Asn Ser Asn
1 5 10

<210> 83
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 83
Gly Tyr Met His Lys Thr Ile Lys Lys Glu Ile Gln Asp
1 5 10

<210> 84
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 84
Ser Thr Cys Thr Asn Ser Thr Arg Glu Ser Asn Ser Ser His
1 5 10

<210> 85
<211> 14
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 85

Thr Gly Thr Ser Glu Ser Ser Val Glu Ala Arg Gly Ser Glu
1 5 10

<210> 86

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 86

Gly Lys Glu Gly Ser Thr Lys Val Glu Glu Asn Ser Met Lys
1 5 10

<210> 87

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 87

Asp Asp Ile Asn Phe Ser Glu Asp Asp Val Glu Ala Val Asn
1 5 10

<210> 88

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 88

Pro Pro Lys Glu Asp Ser His Pro Asp Leu Pro Gly Thr Glu
1 5 10

<210> 89
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 89
Leu Leu Tyr Asn Val Lys Arg His Ser Leu Glu Val Arg Val
1 5 10

<210> 90
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 90
Ser Leu Pro Pro Ser Arg Arg Asn Ser Asn Ser Asn Pro Pro
1 5 10

<210> 91
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 91
Thr Ser Thr Cys Thr Asn Ser Thr Arg Glu Ser Asn Ser Ser
1 5 10

<210> 92
<211> 14

<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 92

Ser Thr Arg Glu Ser Asn Ser Ser His Thr Cys Met Pro Leu
1 5 10

<210> 93

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 93

Gly Glu Asp Asp Ile Asn Phe Ser Glu Asp Asp Val Glu Ala
1 5 10

<210> 94

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 94

Ile Ser Leu Ala His Gly Ile Ile Arg Ser Thr Val Leu Val Ile Phe
1 5 10 15

<210> 95

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 95
Cys Ser Met Ile Trp Gly Ala Ser Pro Ser Tyr Thr Ile Leu Ser Val
1 5 10 15

<210> 96
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 96
Met Glu Ala Lys Asp Gly Ser Leu Lys Ala Lys Glu Gly Ser Thr Gly
1 5 10 15

<210> 97
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 97
Leu Lys Ala Lys Glu Gly Ser Thr Gly Thr Ser Glu Ser Ser Val Glu
1 5 10 15

<210> 98
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 98
Lys Glu Gly Ser Thr Gly Thr Ser Glu Ser Ser Val Glu Ala Arg Gly
1 5 10 15

<210> 99
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 99
Thr Val Ala Ser Asp Gly Ser Met Glu Gly Lys Glu Gly Ser Thr Lys
1 5 10 15

<210> 100
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 100
His Pro Asp Leu Pro Gly Thr Glu Gly Gly Thr Glu Gly Lys Ile Val
1 5 10 15

<210> 101
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 101
Leu Pro Gly Thr Glu Gly Gly Thr Glu Gly Lys Ile Val Pro Ser Tyr
1 5 10 15

<210> 102
<211> 21
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 102

Ser Val Val Ser Phe Ile Val Ile Pro Leu Ile Val Met Ile Ala Cys

1

5

10

15

Tyr Ser Val Val Phe

20